

SEQUENCE LISTING

<110> Washington State University Research Foundation
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Robert, Long

<120> P450 OXYGENASES AND METHODS OF USE

<130> 4630-66380-02

<150> US 60/489,597

<151> 2003-07-22

<160> 41

<170> PatentIn version 3.2

<210> 1

<211> 1688

<212> DNA

<213> Taxus cuspidata

<220>

<221> CDS

<222> (40)..(1548)

<223> coding sequence

<400> 1

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aag agc aca gtt gca aaa ttt aat gag gtc aca cag ctg gac tgt tcc      102
Lys Ser Thr Val Ala Lys Phe Asn Glu Val Thr Gln Leu Asp Cys Ser
              10              15              20

act gaa tct ttt tcc att gcc ctc tca gct att gct ggt att ctt ctg      150
Thr Glu Ser Phe Ser Ile Ala Leu Ser Ala Ile Ala Gly Ile Leu Leu
              25              30              35

ctt ctc ctg ctc ttc cgt tct aaa cgc cac tcc tcc ctt aaa ctt cct      198
Leu Leu Leu Leu Phe Arg Ser Lys Arg His Ser Ser Leu Lys Leu Pro
              40              45              50

cct ggg aaa tta ggc atc cct ttc att ggc gag tcg ttt atc ttc ctg      246
Pro Gly Lys Leu Gly Ile Pro Phe Ile Gly Glu Ser Phe Ile Phe Leu
              55              60              65

agg gct ctt cga tcg aac tcg ctg gag caa ttt ttt gac gag aga gtg      294
Arg Ala Leu Arg Ser Asn Ser Leu Glu Gln Phe Phe Asp Glu Arg Val
              70              75              80              85

aag aaa ttc ggc ctc gtg ttc aag acc tcc ttg att ggg cat ccc aca      342
Lys Lys Phe Gly Leu Val Phe Lys Thr Ser Leu Ile Gly His Pro Thr
              90              95              100

gta gta ctc tgc ggc cct gcg gga aac cgg ctt att ctg tcc aac gag      390
Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu Ile Leu Ser Asn Glu
              105              110              115

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gag aag ctg gtg cag atg tcg tgg ccc gct caa ttt atg aag ctc atg Glu Lys Leu Val Gln Met Ser Trp Pro Ala Gln Phe Met Lys Leu Met 120 125 130	438
ggg gag aat tcc gtt gcc acc agg agg ggt gaa gac cat ata gtt atg Gly Glu Asn Ser Val Ala Thr Arg Arg Gly Glu Asp His Ile Val Met 135 140 145	486
cgc tct gct ctt gca ggt ttt ttc ggc cct ggt gcg ctg cag agt tac Arg Ser Ala Leu Ala Gly Phe Phe Gly Pro Gly Ala Leu Gln Ser Tyr 150 155 160 165	534
att ggt aaa atg aat aca gag atc cag agt cat atc aac gaa aaa tgg Ile Gly Lys Met Asn Thr Glu Ile Gln Ser His Ile Asn Glu Lys Trp 170 175 180	582
aag gga aaa gat gag gtg aat gta ctt cct ttg gta aga gag ctc gtc Lys Gly Lys Asp Glu Val Asn Val Leu Pro Leu Val Arg Glu Leu Val 185 190 195	630
ttc aac att tcg gcc atc ttg ttt ttc aac ata tat gat aag cag gaa Phe Asn Ile Ser Ala Ile Leu Phe Phe Asn Ile Tyr Asp Lys Gln Glu 200 205 210	678
cag gat cgt ctg cat aag ctt ttg gaa act att ctg gtc gga agt ttt Gln Asp Arg Leu His Lys Leu Leu Glu Thr Ile Leu Val Gly Ser Phe 215 220 225	726
gct ctt ccg att gac ttg ccc gga ttt ggt ttc cat aga gca ctc cag Ala Leu Pro Ile Asp Leu Pro Gly Phe Gly Phe His Arg Ala Leu Gln 230 235 240 245	774
gga cgg gcc aag ctc aac aaa att atg ctg tct tta att aaa aag aga Gly Arg Ala Lys Leu Asn Lys Ile Met Leu Ser Leu Ile Lys Lys Arg 250 255 260	822
aaa gaa gat ctg cag tct gga tcg gca aca gcc acg cag gat ctg ctc Lys Glu Asp Leu Gln Ser Gly Ser Ala Thr Ala Thr Gln Asp Leu Leu 265 270 275	870
tct gtt ttg ctc act ttc aga gat gac aaa ggg act cca ctc acc aat Ser Val Leu Leu Thr Phe Arg Asp Asp Lys Gly Thr Pro Leu Thr Asn 280 285 290	918
gat gag ata ctc gac aac ttt tct tct ctg ctc cat gcc tcc tat gac Asp Glu Ile Leu Asp Asn Phe Ser Ser Leu Leu His Ala Ser Tyr Asp 295 300 305	966
acc acc act tcg cca atg gct ttg att ttc aag ctc ttg tct tcc aat Thr Thr Thr Ser Pro Met Ala Leu Ile Phe Lys Leu Leu Ser Ser Asn 310 315 320 325	1014
cca gaa tgc tat caa aaa gta gtt caa gag caa ttg gag ata ctt tcc Pro Glu Cys Tyr Gln Lys Val Val Gln Glu Gln Leu Glu Ile Leu Ser 330 335 340	1062
aac aaa gag gag gcc gaa gaa atc aca tgg aag gat ctc aaa gcc atg Asn Lys Glu Glu Gly Glu Glu Ile Thr Trp Lys Asp Leu Lys Ala Met 345 350 355	1110

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aaa tac aca tgg caa gta gct cag gaa acg ctg cgg atg ttt cct cca      1158
Lys Tyr Thr Trp Gln Val Ala Gln Glu Thr Leu Arg Met Phe Pro Pro
      360                      365                      370

gtt ttc gga aca ttt cgc aag gcc atc act gac att cag tat gat ggt      1206
Val Phe Gly Thr Phe Arg Lys Ala Ile Thr Asp Ile Gln Tyr Asp Gly
      375                      380                      385

tac aca att cca aaa ggg tgg aag ctg ttg tgg aca act tac agt aca      1254
Tyr Thr Ile Pro Lys Gly Trp Lys Leu Leu Trp Thr Thr Tyr Ser Thr
      390                      395                      400                      405

cat ccc aag gac ttg tat ttc aat gaa cca gag aaa ttc atg cct tca      1302
His Pro Lys Asp Leu Tyr Phe Asn Glu Pro Glu Lys Phe Met Pro Ser
      410                      415                      420

aga ttc gat cag gaa gga aag cat gta gct cct tac aca ttt ttg ccc      1350
Arg Phe Asp Gln Glu Gly Lys His Val Ala Pro Tyr Thr Phe Leu Pro
      425                      430                      435

ttc ggt gga ggc caa cgg tca tgt gtg gga tgg gaa ttt tca aag atg      1398
Phe Gly Gly Gly Gln Arg Ser Cys Val Gly Trp Glu Phe Ser Lys Met
      440                      445                      450

gag ata tta cta ttc gtt cat cat ttt gtc aaa act ttt agc agc tac      1446
Glu Ile Leu Leu Phe Val His His Phe Val Lys Thr Phe Ser Ser Tyr
      455                      460                      465

acc cca gtt gat ccc gac gaa aaa ata tca ggg gat cca ctc cct cct      1494
Thr Pro Val Asp Pro Asp Glu Lys Ile Ser Gly Asp Pro Leu Pro Pro
      470                      475                      480                      485

ctt cct tcc aag gga ttt tcc att aaa ctg ttt ccc gag acc ata gtc      1542
Leu Pro Ser Lys Gly Phe Ser Ile Lys Leu Phe Pro Glu Thr Ile Val
      490                      495                      500

aat tga aggagaaaaac cacagtgcag aactgctatt cttgaatcct cgctcaagaa      1598
Asn

taatacaaac atgcatcacc aacaatgttt atgcactcaa tgcaaattaa cagtgtgtca      1658

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 <211> 502
 <212> PRT
 <213> *Taxus cuspidata*

<400> 2

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Gln Leu Asp Cys Ser Thr Glu Ser Phe Ser Ile Ala Leu Ser Ala Ile
20          25          30

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Ala Gly Ile Leu Leu Leu Leu Leu Leu Phe Arg Ser Lys Arg His Ser

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35	40	45
Ser Leu Lys Leu Pro Pro Gly Lys Leu Gly Ile Pro Phe Ile Gly Glu 50 55 60		
Ser Phe Ile Phe Leu Arg Ala Leu Arg Ser Asn Ser Leu Glu Gln Phe 65 70 75 80		
Phe Asp Glu Arg Val Lys Lys Phe Gly Leu Val Phe Lys Thr Ser Leu 85 90 95		
Ile Gly His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu 100 105 110		
Ile Leu Ser Asn Glu Glu Lys Leu Val Gln Met Ser Trp Pro Ala Gln 115 120 125		
Phe Met Lys Leu Met Gly Glu Asn Ser Val Ala Thr Arg Arg Gly Glu 130 135 140		
Asp His Ile Val Met Arg Ser Ala Leu Ala Gly Phe Phe Gly Pro Gly 145 150 155 160		
Ala Leu Gln Ser Tyr Ile Gly Lys Met Asn Thr Glu Ile Gln Ser His 165 170 175		
Ile Asn Glu Lys Trp Lys Gly Lys Asp Glu Val Asn Val Leu Pro Leu 180 185 190		
Val Arg Glu Leu Val Phe Asn Ile Ser Ala Ile Leu Phe Phe Asn Ile 195 200 205		
Tyr Asp Lys Gln Glu Gln Asp Arg Leu His Lys Leu Leu Glu Thr Ile 210 215 220		
Leu Val Gly Ser Phe Ala Leu Pro Ile Asp Leu Pro Gly Phe Gly Phe 225 230 235 240		
His Arg Ala Leu Gln Gly Arg Ala Lys Leu Asn Lys Ile Met Leu Ser 245 250 255		
Leu Ile Lys Lys Arg Lys Glu Asp Leu Gln Ser Gly Ser Ala Thr Ala 260 265 270		
Thr Gln Asp Leu Leu Ser Val Leu Leu Thr Phe Arg Asp Asp Lys Gly 275 280 285		

Thr Pro Leu Thr Asn Asp Glu Ile Leu Asp Asn Phe Ser Ser Leu Leu
 290 295 300

His Ala Ser Tyr Asp Thr Thr Thr Ser Pro Met Ala Leu Ile Phe Lys
 305 310 315 320

Leu Leu Ser Ser Asn Pro Glu Cys Tyr Gln Lys Val Val Gln Glu Gln
 325 330 335

Leu Glu Ile Leu Ser Asn Lys Glu Glu Gly Glu Glu Ile Thr Trp Lys
 340 345 350

Asp Leu Lys Ala Met Lys Tyr Thr Trp Gln Val Ala Gln Glu Thr Leu
 355 360 365

Arg Met Phe Pro Pro Val Phe Gly Thr Phe Arg Lys Ala Ile Thr Asp
 370 375 380

Ile Gln Tyr Asp Gly Tyr Thr Ile Pro Lys Gly Trp Lys Leu Leu Trp
 385 390 395 400

Thr Thr Tyr Ser Thr His Pro Lys Asp Leu Tyr Phe Asn Glu Pro Glu
 405 410 415

Lys Phe Met Pro Ser Arg Phe Asp Gln Glu Gly Lys His Val Ala Pro
 420 425 430

Tyr Thr Phe Leu Pro Phe Gly Gly Gly Gln Arg Ser Cys Val Gly Trp
 435 440 445

Glu Phe Ser Lys Met Glu Ile Leu Leu Phe Val His His Phe Val Lys
 450 455 460

Thr Phe Ser Ser Tyr Thr Pro Val Asp Pro Asp Glu Lys Ile Ser Gly
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Asp Pro Leu Pro Pro Leu Pro Ser Lys Gly Phe Ser Ile Lys Leu Phe
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Pro Glu Thr Ile Val Asn
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<210> 3
 <211> 1455
 <212> DNA

<213> *Taxus cuspidata*

<400> 3

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cttccccctg gaaacatggg cttccctctc attggggaga ctatagcact tatatcagat      180
acacctcgga agtttatcga cgacagagtg aagaaattcg gcctgggttt caagacttcg      240
ctaattgggc atcccgcagt tgtaatatgc ggctcctccg caaaccgttt cctcctctcc      300
aacgaggaaa agctgggtgc gatgtctttg cccaacgcag tactgaaact cttggggcag      360
gattgcgtta tggggaaaaac cggagtgagg catgggattg tacgtaccgc actagccgcg      420
gccttggggc ccagggcggt gcagaattat gtggccaaaa tgagttcaga gatcgaacac      480
catatcaacc aaaaatggaa ggggaaagat gaggtgaagg tgcttctctc gataagaagc      540
ctcgtcttct ccatttcaac cagcttggtt ttcgggtataa acgatgagca ccaacagaag      600
cgacttcacg atcttttggg aactgtagct atgggacttg tgagtattcc cctagacttt      660
ccaggaactc gttttcgtaa agcactttac gcgcggtcga agctcgatga aattatgtct      720
tctgtaatag aaaggagaag aagcgatctt cgttcaggag cagcttcaag cgaccaagat      780
ctactgtcgg tgttggtcac cttcaaagat gaaagaggga attcattcgc agacaaggag      840
atactggata acttctcttt tctacttcac gccttatacg acaccacaat ttcaccactc      900
accttgatat ttaagctgct ctctcttagt cctgaatgct atgagaatat agctcaagag      960
cagctggaaa tacttgcaa taaaaaggat agagaggaaa tcagctggaa ggatctgaag     1020
gatatgaaat atacatggca agcagttcag gaaactttga ggatgttccc tccagtttat     1080
ggatatattc gcgaggcttt gacagatatt gactatgatg gctatacaat accaaaagga     1140
tggaagaatat tatgttcacc tcatactacg catagtaaag aggagtattt cgatgagccg     1200
gaagaattca gaccttcaag attcgaggat caaggaaggc atgtggctcc ttacacattc     1260
ataccatttg gaggaggcct gcgcactctg gcaggctggg aatttgcaaa gatggagata     1320
ttactgttta tgcattcatt tggtaaaact ttcagtcact tcattccagt tgaccccaac     1380
gaaaagattt cgagagatcc actgcctccc atccctgtca aaggattttc cataaagcct     1440
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1455

<210> 4

<211> 484

<212> PRT

<213> *Taxus cuspidata*

<400> 4

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 20 25 30
 Lys Gln Tyr Arg Ser Ser Arg Lys Leu Pro Pro Gly Asn Met Gly Phe
 35 40 45
 Pro Leu Ile Gly Glu Thr Ile Ala Leu Ile Ser Asp Thr Pro Arg Lys
 50 55 60
 Phe Ile Asp Asp Arg Val Lys Lys Phe Gly Leu Val Phe Lys Thr Ser
 65 70 75 80
 Leu Ile Gly His Pro Ala Val Val Ile Cys Gly Ser Ser Ala Asn Arg
 85 90 95
 Phe Leu Leu Ser Asn Glu Glu Lys Leu Val Arg Met Ser Leu Pro Asn
 100 105 110
 Ala Val Leu Lys Leu Leu Gly Gln Asp Cys Val Met Gly Lys Thr Gly
 115 120 125
 Val Glu His Gly Ile Val Arg Thr Ala Leu Ala Arg Ala Leu Gly Pro
 130 135 140
 Gln Ala Leu Gln Asn Tyr Val Ala Lys Met Ser Ser Glu Ile Glu His
 145 150 155 160
 His Ile Asn Gln Lys Trp Lys Gly Lys Asp Glu Val Lys Val Leu Pro
 165 170 175
 Leu Ile Arg Ser Leu Val Phe Ser Ile Ser Thr Ser Leu Phe Phe Gly
 180 185 190
 Ile Asn Asp Glu His Gln Gln Lys Arg Leu His His Leu Leu Glu Thr
 195 200 205
 Val Ala Met Gly Leu Val Ser Ile Pro Leu Asp Phe Pro Gly Thr Arg
 210 215 220
 Phe Arg Lys Ala Leu Tyr Ala Arg Ser Lys Leu Asp Glu Ile Met Ser
 225 230 235 240
 Ser Val Ile Glu Arg Arg Arg Ser Asp Leu Arg Ser Gly Ala Ala Ser

245	250	255
Ser Asp Gln Asp Leu Leu Ser Val	Leu Val Thr Phe Lys Asp Glu Arg	
260	265	270
Gly Asn Ser Phe Ala Asp Lys Glu Ile Leu Asp Asn Phe Ser Phe Leu		
275	280	285
Leu His Ala Leu Tyr Asp Thr Thr Ile Ser Pro Leu Thr Leu Ile Phe		
290	295	300
Lys Leu Leu Ser Ser Ser Pro Glu Cys Tyr Glu Asn Ile Ala Gln Glu		
305	310	315
Gln Leu Glu Ile Leu Gly Asn Lys Lys Asp Arg Glu Glu Ile Ser Trp		
325	330	335
Lys Asp Leu Lys Asp Met Lys Tyr Thr Trp Gln Ala Val Gln Glu Thr		
340	345	350
Leu Arg Met Phe Pro Pro Val Tyr Gly Tyr Ile Arg Glu Ala Leu Thr		
355	360	365
Asp Ile Asp Tyr Asp Gly Tyr Thr Ile Pro Lys Gly Trp Arg Ile Leu		
370	375	380
Cys Ser Pro His Thr Thr His Ser Lys Glu Glu Tyr Phe Asp Glu Pro		
385	390	395
Glu Glu Phe Arg Pro Ser Arg Phe Glu Asp Gln Gly Arg His Val Ala		
405	410	415
Pro Tyr Thr Phe Ile Pro Phe Gly Gly Gly Leu Arg Ile Cys Ala Gly		
420	425	430
Trp Glu Phe Ala Lys Met Glu Ile Leu Leu Phe Met His His Phe Val		
435	440	445
Lys Thr Phe Ser His Phe Ile Pro Val Asp Pro Asn Glu Lys Ile Ser		
450	455	460
Arg Asp Pro Leu Pro Pro Ile Pro Val Lys Gly Phe Ser Ile Lys Pro		
465	470	475
Phe Pro Arg Ser		

<210> 5
 <211> 1455
 <212> DNA
 <213> *Taxus cuspidata*

<400> 5
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 cttccccctg gaaacatggg cttccctctc attggggaga cgatagcact ggcatcacag 180
 acacctgata aatttttcgg cgatagaatg aagaaattcg gcaagggttt caagacttcg 240
 ttaattgggc atcccacaat tgtgctctgc gggttcctccg gaaaccgttt tctcctctcc 300
 aacgaggaaa aactggtgcg gatgtttccg cccaactcat ccagcaaact cctggggcag 360
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 tgtttgggcc cccaagcgt gcagaattac gtgtccaaaa tgagttcaga gatccaacgt 480
 catatcaacc aaaaatggaa gggaaaagggt gaagtgaaga tgcttcctct gataagaagc 540
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 gttcccagat cctaa 1455

<210> 6
 <211> 484

<212> PRT

<213> *Taxus cuspidata*

<400> 6

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Leu Leu Ser Leu Thr Leu Thr Leu Ile Leu Leu Phe Ile Phe Cys Ser
 20 25 30

Lys Gln Tyr Arg Ser Ser Leu Lys Leu Pro Pro Gly Asn Met Gly Phe
 35 40 45

Pro Leu Ile Gly Glu Thr Ile Ala Leu Ala Ser Gln Thr Pro Asp Lys
 50 55 60

Phe Phe Gly Asp Arg Met Lys Lys Phe Gly Lys Val Phe Lys Thr Ser
 65 70 75 80

Leu Ile Gly His Pro Thr Ile Val Leu Cys Gly Ser Ser Gly Asn Arg
 85 90 95

Phe Leu Leu Ser Asn Glu Glu Lys Leu Val Arg Met Phe Pro Pro Asn
 100 105 110

Ser Ser Ser Lys Leu Leu Gly Gln Asp Ser Val Leu Gly Lys Ile Gly
 115 120 125

Glu Glu His Arg Ile Val Arg Thr Ala Leu Ala Arg Cys Leu Gly Pro
 130 135 140

Gln Ala Leu Gln Asn Tyr Val Ser Lys Met Ser Ser Glu Ile Gln Arg
 145 150 155 160

His Ile Asn Gln Lys Trp Lys Gly Lys Gly Glu Val Lys Met Leu Pro
 165 170 175

Leu Ile Arg Ser Leu Val Phe Ser Ile Ala Thr Ser Leu Phe Phe Gly
 180 185 190

Ile Thr Asp Glu Gln Gln Gln Glu Arg Leu His His Leu Leu Glu Thr
 195 200 205

Val Val Thr Gly Leu Leu Cys Ile Pro Leu Asp Phe Pro Gly Thr Thr
 210 215 220

Phe Arg Lys Ala Leu His Ala Arg Ser Lys Leu Asp Glu Ile Met Ser
 225 230 235 240
 Ser Val Ile Glu Arg Arg Arg Asn Asp Leu Arg Leu Gly Ala Ala Ser
 245 250 255
 Ser Asp Gln Asp Leu Leu Ser Val Leu Leu Thr Phe Lys Asp Glu Arg
 260 265 270
 Gly Asn Pro Phe Ala Asp Lys Glu Ile Leu Asp Asn Phe Ser Phe Leu
 275 280 285
 Leu His Ala Leu Tyr Asp Thr Thr Ile Ser Pro Leu Thr Leu Val Phe
 290 295 300
 Lys Leu Val Ser Ser Asn Pro Glu Cys Tyr Glu Asn Ile Ala Gln Glu
 305 310 315 320
 Gln Leu Glu Ile Leu Arg Asn Lys Lys Asp Gly Glu Asp Ile Ser Trp
 325 330 335
 Ala Asp Leu Lys Asp Met Lys Tyr Thr Trp Gln Ala Val Gln Glu Thr
 340 345 350
 Leu Arg Met Cys Pro Pro Val Tyr Gly Asn Phe Arg Lys Ala Leu Thr
 355 360 365
 Asp Ile His Tyr Asp Gly Tyr Thr Ile Pro Lys Gly Trp Arg Ile Leu
 370 375 380
 Cys Ser Pro Tyr Thr Thr His Ser Lys Glu Glu Tyr Phe Asp Asp Pro
 385 390 395 400
 Glu Lys Phe Arg Pro Ser Arg Phe Glu Glu Gln Gly Arg Asp Val Ala
 405 410 415
 Pro Tyr Thr Phe Ile Pro Phe Gly Gly Gly Leu Arg Ile Cys Pro Gly
 420 425 430
 Arg Glu Phe Ala Lys Met Glu Ile Leu Val Phe Met His His Phe Val
 435 440 445
 Lys Ala Phe Ser Ser Phe Ile Pro Val Asp Pro Asn Glu Lys Ile Ser
 450 455 460
 Thr Asp Pro Leu Pro Ser Ile Pro Val Asn Gly Phe Ser Ile Asn Leu

465

470

475

480

Val Pro Arg Ser

<210> 7

<211> 1503

<212> DNA

<213> *Taxus cuspidata*

<400> 7

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ctcgtcatca cttctaaacg ccgttcctct cttaaacctc ctcttgaaa actaggcctc      180
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aaatggaagg gaaaagatga agtgaatgta ctgagtttgg taagagatct tgtcatggac      600
aattcagcta tcttggtttt caatatatac gataaagagc gaaagcaaca actgcatgaa      660
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tga 1503

<210> 8

<211> 500

<212> PRT

<213> *Taxus cuspidata*

<400> 8

Met Asp Ala Leu Ser Leu Val Asn Ser Thr Val Ala Lys Phe Asn Glu
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20 25 30

Ala Ile Ala Gly Ile Ile Val Leu Leu Val Ile Thr Ser Lys Arg Arg
35 40 45

Ser Ser Leu Lys Leu Pro Pro Gly Lys Leu Gly Leu Pro Phe Ile Gly
50 55 60

Glu Thr Leu Glu Phe Val Lys Ala Leu Arg Ser Asp Thr Leu Arg Gln
65 70 75 80

Phe Val Glu Glu Arg Glu Gly Lys Phe Gly Arg Val Phe Lys Thr Ser
85 90 95

Leu Leu Gly Lys Pro Thr Val Ile Leu Cys Gly Pro Ala Gly Asn Arg
100 105 110

Leu Val Leu Ser Asn Glu Glu Lys Leu Leu His Val Ser Trp Ser Ala
115 120 125

Gln Ile Ala Arg Ile Leu Gly Leu Asn Ser Val Ala Val Lys Arg Gly
130 135 140

Asp Asp His Arg Val Leu Arg Val Ala Leu Ala Gly Phe Leu Gly Ser
145 150 155 160

Ala Gly Leu Gln Leu Tyr Ile Gly Lys Met Ser Ala Leu Ile Arg Asn
165 170 175

His Ile Asn Glu Lys Trp Lys Gly Lys Asp Glu Val Asn Val Leu Ser
180 185 190

Leu Val Arg Asp Leu Val Met Asp Asn Ser Ala Ile Leu Phe Phe Asn

195					200					205					
Ile	Tyr	Asp	Lys	Glu	Arg	Lys	Gln	Gln	Leu	His	Glu	Ile	Leu	Lys	Ile
210						215					220				
Ile	Leu	Ala	Ser	His	Phe	Gly	Ile	Pro	Leu	Asn	Ile	Pro	Gly	Phe	Leu
225					230					235					240
Tyr	Arg	Lys	Ala	Leu	Lys	Gly	Ser	Leu	Lys	Arg	Lys	Lys	Ile	Leu	Ser
				245					250					255	
Ala	Leu	Leu	Glu	Lys	Arg	Lys	Asp	Glu	Leu	Arg	Ser	Arg	Leu	Ala	Ser
			260					265					270		
Ser	Asn	Gln	Asp	Leu	Leu	Ser	Val	Leu	Leu	Ser	Phe	Arg	Asp	Glu	Arg
			275				280					285			
Gly	Lys	Pro	Leu	Ser	Asp	Glu	Ala	Val	Leu	Asp	Asn	Cys	Phe	Ala	Met
290					295						300				
Leu	Asp	Ala	Ser	Tyr	Asp	Thr	Thr	Thr	Ser	Gln	Met	Thr	Leu	Ile	Leu
305					310					315					320
Lys	Met	Leu	Ser	Ser	Asn	Pro	Glu	Cys	Phe	Glu	Lys	Val	Val	Gln	Glu
				325					330					335	
Gln	Leu	Glu	Ile	Ala	Ser	Asn	Lys	Lys	Glu	Gly	Glu	Glu	Ile	Thr	Met
			340					345					350		
Lys	Asp	Ile	Lys	Ala	Met	Lys	Tyr	Thr	Trp	Gln	Val	Leu	Gln	Glu	Ser
		355					360					365			
Leu	Arg	Met	Leu	Ser	Pro	Val	Phe	Gly	Thr	Leu	Arg	Lys	Thr	Met	Asn
	370					375					380				
Asp	Ile	Asn	His	Asp	Gly	Tyr	Thr	Ile	Pro	Lys	Gly	Trp	Gln	Val	Val
385					390					395					400
Trp	Thr	Thr	Tyr	Ser	Thr	His	Gln	Lys	Asp	Ile	Tyr	Phe	Lys	Gln	Pro
				405					410					415	
Asp	Lys	Phe	Met	Pro	Ser	Arg	Phe	Glu	Glu	Glu	Asp	Gly	His	Leu	Asp
			420					425					430		
Ala	Tyr	Thr	Phe	Val	Pro	Phe	Gly	Gly	Gly	Arg	Arg	Thr	Cys	Pro	Gly
	435						440					445			

Trp Glu Tyr Ala Lys Val Glu Ile Leu Leu Phe Leu His His Phe Val
 450 455 460

Lys Ala Phe Ser Gly Tyr Thr Pro Thr Asp Pro His Glu Arg Ile Cys
 465 470 475 480

Gly Tyr Pro Val Pro Leu Val Pro Val Lys Gly Phe Pro Ile Lys Leu
 485 490 495

Ile Ala Arg Ser
 500

<210> 9
 <211> 1476
 <212> DNA
 <213> *Taxus cuspidata*

<220>
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 <222> (68)..(68)
 <223> n is a, c, g, or t

<220>
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 <222> (510)..(510)
 <223> n is a, c, g, or t

<220>
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 <222> (1092)..(1092)
 <223> n is a, c, g, or t

<220>
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 <222> (1100)..(1100)
 <223> n is a, c, g, or t

<220>
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 <222> (1188)..(1188)
 <223> n is a, c, g, or t

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 cgacgatcct atgtgaatct cccccctgga aatttaggtt tacctttcat tggcgagacg 180
 atacagttct tggggggcact tcagtcagaa aaaccccata catttttcga tgagagagtg 240
 aagaaattcg gtaagggtctt caagacttct ctaattgggg atcccacggt ggtactctgc 300
 gggccggcgg gaaaccgctt agttctgtcg aacgaagaca agctgggtgca gtccgcaggg 360

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cccaagtctt tcctgaaact gtttggggag gattccgttg cggccaaaag agaagagagc 420
catcgcatct tacgttcggc tctgggtcga tttctgggtc cccatgcttt acagaattat 480
attgggaaaa tgaattcaga aatgcaacgn catttcgatg acaaattggaa gggaaaagat 540
gaggtgaagg tgcttccttt ggtagaggc ctcattttct ccattgctac ctccctgttc 600
ttcaatataa atgatgacag acaacgtgag caactccatg gtctgctgga tacaatactt 660
gtgggaagta tgactattcc tctgaacatt ccaggaactc tttttcgtaa agctgtcaag 720
gcacgggcga agctggacga aattcttttt gctttgatag agaacagaag aagagagctg 780
agatcgggcc taaattctgg taatcaagat cttctgtcgt ccttgctcac cttcaaagat 840
gaaaaaggga atccactgac agacaaggag atcctcgaca acttctctgt tatgcttcat 900
gcctcgtatg acactactgt ttcaccaacg gtcttgatat tgaagcttct cgcctccaat 960
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gaaccctaa gnatgccccn ccagcttttg gaatgtttcg aagagctttc cctgatattc 1140
agttggaagg ctatacaatt ccaaaaggat gggcaattgt gtggccanct tatagtcaat 1200
gggagagaag agttcttcaa tgaaccagac aaattcaagc cttccagatt cgaggaagga 1260
aagccctgg atccttacac attcatacca ttcggagcag gggtagcat atgtgcagga 1320
tggaatttg caaaggctga actattactg tttgtccatc ctttggttaa aaacttcagc 1380
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accagtggac aactcatgaa acttattccg agatca 1476

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<210> 10
<211> 500
<212> PRT
<213> Taxus cuspidata

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<220>
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<222> (23)..(23)
<223> Xaa can be any naturally occurring amino acid

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<220>
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<222> (366)..(366)
<223> Xaa can be any naturally occurring amino acid

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<220>
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<222> (371)..(371)
<223> Xaa can be any naturally occurring amino acid

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<220>

<221> misc_feature

<222> (402)..(402)

<223> Xaa can be any naturally occurring amino acid

<400> 10

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Ser Pro Leu Ile Ile Ser Xaa Ala Ala Ala Leu Ala Ala Phe Leu Gly
 20 25 30

Ile Val Ile Phe Ser Ile Phe Ser Ser Thr Arg Arg Ser Tyr Val Asn
 35 40 45

Leu Pro Pro Gly Asn Leu Gly Leu Pro Phe Ile Gly Glu Thr Ile Gln
 50 55 60

Phe Leu Gly Ala Leu Gln Ser Glu Lys Pro His Thr Phe Phe Asp Glu
 65 70 75 80

Arg Val Lys Lys Phe Gly Lys Val Phe Lys Thr Ser Leu Ile Gly Asp
 85 90 95

Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu Val Leu Ser
 100 105 110

Asn Glu Asp Lys Leu Val Gln Ser Ala Gly Pro Lys Ser Phe Leu Lys
 115 120 125

Leu Phe Gly Glu Asp Ser Val Ala Ala Lys Arg Glu Glu Ser His Arg
 130 135 140

Ile Leu Arg Ser Ala Leu Gly Arg Phe Leu Gly Pro His Ala Leu Gln
 145 150 155 160

Asn Tyr Ile Gly Lys Met Asn Ser Glu Met Gln Arg His Phe Asp Asp
 165 170 175

Lys Trp Lys Gly Lys Asp Glu Val Lys Val Leu Pro Leu Val Arg Gly
 180 185 190

Leu Ile Phe Ser Ile Ala Thr Ser Leu Phe Phe Asn Ile Asn Asp Asp
 195 200 205

Arg Gln Arg Glu Gln Leu His Gly Leu Leu Asp Thr Ile Leu Val Gly
 210 215 220

Ser Met Thr Ile Pro Leu Asn Ile Pro Gly Thr Leu Phe Arg Lys Ala
 225 230 235 240
 Val Lys Ala Arg Ala Lys Leu Asp Glu Ile Leu Phe Ala Leu Ile Glu
 245 250 255
 Asn Arg Arg Arg Glu Leu Arg Ser Gly Leu Asn Ser Gly Asn Gln Asp
 260 265 270
 Leu Leu Ser Ser Leu Leu Thr Phe Lys Asp Glu Lys Gly Asn Pro Leu
 275 280 285
 Thr Asp Lys Glu Ile Leu Asp Asn Phe Ser Val Met Leu His Ala Ser
 290 295 300
 Tyr Asp Thr Thr Val Ser Pro Thr Val Leu Ile Leu Lys Leu Leu Ala
 305 310 315 320
 Ser Asn Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Gly Ile
 325 330 335
 Leu Ala Ser Lys Lys Glu Gly Glu Glu Val Asn Trp Lys Asp Leu Lys
 340 345 350
 Ala Met Pro Tyr Thr Trp Gln Ala Ile Gln Glu Pro Leu Xaa Ala Ala
 355 360 365
 Met Pro Xaa Ala Ala Gln Leu Leu Glu Cys Phe Glu Glu Leu Ser Leu
 370 375 380
 Ile Phe Ser Trp Lys Ala Ile Gln Phe Gln Lys Asp Gly Gln Leu Cys
 385 390 395 400
 Gly Xaa Ala Ala Leu Ile Val Asn Gly Arg Glu Glu Phe Phe Asn Glu
 405 410 415
 Pro Asp Lys Phe Lys Pro Ser Arg Phe Glu Glu Gly Lys Pro Leu Asp
 420 425 430
 Pro Tyr Thr Phe Ile Pro Phe Gly Ala Gly Val Arg Ile Cys Ala Gly
 435 440 445
 Trp Glu Phe Ala Lys Ala Glu Leu Leu Leu Phe Val His Pro Phe Val
 450 455 460

Lys Asn Phe Ser Gly Cys Ile Ile Ile Asp Pro Asn Glu Lys Ile Ser
 465 470 475 480

Gly Asp Pro Phe Pro Pro Leu Pro Thr Ser Gly Gln Leu Met Lys Leu
 485 490 495

Ile Pro Arg Ser
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<210> 11
 <211> 1530
 <212> DNA
 <213> *Taxus cuspidata*

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 cggttctaaac gccgttcctc tgttggacta cccccaggga aattagggtta ccctttcatt 180
 ggcgagtcgt tactgttcct gaaggctctt cgatcaaaca cagttgaaca atttttggac 240
 gagagagtga agaatttcgg gaatgtcttc aagacgtcat taattgggca tccgacagta 300
 gttctctgcg ggcctgcagg aaaccggcta atcctggcga acgaggagaa gctgggtgcag 360
 atgtcgtggc ccaaatactc tatgaaactc atgggggaga agtctattac tgccaaaagg 420
 ggcgaaggcc atatgatcat ccgctccgca ctgcaaggct ttttcagccc tgggtgctctg 480
 cagaaataca taggcctaat gagtaaaaca atagaaaatc atattaatga gaaatggaag 540
 ggaaacgacc aagtgagtgt agttgctttg gtaggagatc tcgtcttcga tatttcggcc 600
 tgtttggtct tcaatataaa tgagaagcat gaacgggaac gactgtttga gcttttgag 660
 attatagctg tcggagtttt ggctgttcctg gtggatcttc ccgggtttgc ttaccatcgg 720
 gcacttcaag cacggtcgaa gcttaatgca attctctccg gtttgataga aaagagaaaa 780
 atggatctga gctcaggatt agcgactagc aatcaggatc ttctttctgt gtttctcacc 840
 ttcaaagatg acagaggaaa tccatgcagc gatgaggaaa tcctcgacaa cttttccggg 900
 ctgcttcatg gatcctatga caccactgtt tcagcaatgg cctgcgtttt taagcttttg 960
 tcttccaatc ccgaatgcta tgaaaaagta gttcaagagc aattggggat actttcgaat 1020
 aaattggaag gagacgaaat cacatggaaa gatgtgaaat ccatgaaata tacatggcaa 1080
 gtcgttcagg aaacgttacg attgtatccg tcaatttttg gatcatttcg ccaggccatc 1140
 actgacattc attataatgg ttacataatt ccaaaagggt ggaagctttt gtggacacca 1200
 tacacaacac atcccaagga aatgtatttc agtgagccgg agaaattcct gccttcgagg 1260

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ttcgatcagg aagggaaact tgtagtcct tacacatttt taccctttgg tggaggccag 1320
cgttcatgtc caggatggga attttcaaag atggagattt tactgtcggg gcatcatttt 1380
gttaaaacat tcagcacctt caccacagtt gaccagcag aaataattgc aagagattcc 1440
ctctgccctc tcccttccaa tgggttttct gtaaaacttt ttcctagatc ctattcactt 1500
cacacaggca accagggtcaa gaaaatataa 1530

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<210> 12
<211> 509
<212> PRT
<213> Taxus cuspidata

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<400> 12

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Met Asp Val Phe Tyr Pro Leu Lys Ser Thr Val Ala Lys Phe Asn Glu
1           5           10           15

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```

Cys Phe Pro Ala Ile Leu Phe Ile Val Leu Ser Ala Val Ala Gly Ile
          20           25           30

```

```

Val Leu Pro Leu Leu Leu Phe Leu Arg Ser Lys Arg Arg Ser Ser Val
          35           40           45

```

```

Gly Leu Pro Pro Gly Lys Leu Gly Tyr Pro Phe Ile Gly Glu Ser Leu
          50           55           60

```

```

Leu Phe Leu Lys Ala Leu Arg Ser Asn Thr Val Glu Gln Phe Leu Asp
65           70           75           80

```

```

Glu Arg Val Lys Asn Phe Gly Asn Val Phe Lys Thr Ser Leu Ile Gly
          85           90           95

```

```

His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu Ile Leu
          100          105          110

```

```

Ala Asn Glu Glu Lys Leu Val Gln Met Ser Trp Pro Lys Ser Ser Met
          115          120          125

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Lys Leu Met Gly Glu Lys Ser Ile Thr Ala Lys Arg Gly Glu Gly His
          130          135          140

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Met Ile Ile Arg Ser Ala Leu Gln Gly Phe Phe Ser Pro Gly Ala Leu
145           150           155           160

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Gln Lys Tyr Ile Gly Gln Met Ser Lys Thr Ile Glu Asn His Ile Asn
          165          170          175

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Glu Lys Trp Lys Gly Asn Asp Gln Val Ser Val Val Ala Leu Val Gly
 180 185 190

Asp Leu Val Phe Asp Ile Ser Ala Cys Leu Phe Phe Asn Ile Asn Glu
 195 200 205

Lys His Glu Arg Glu Arg Leu Phe Glu Leu Leu Glu Ile Ile Ala Val
 210 215 220

Gly Val Leu Ala Val Pro Val Asp Leu Pro Gly Phe Ala Tyr His Arg
 225 230 235 240

Ala Leu Gln Ala Arg Ser Lys Leu Asn Ala Ile Leu Ser Gly Leu Ile
 245 250 255

Glu Lys Arg Lys Met Asp Leu Ser Ser Gly Leu Ala Thr Ser Asn Gln
 260 265 270

Asp Leu Leu Ser Val Phe Leu Thr Phe Lys Asp Asp Arg Gly Asn Pro
 275 280 285

Cys Ser Asp Glu Glu Ile Leu Asp Asn Phe Ser Gly Leu Leu His Gly
 290 295 300

Ser Tyr Asp Thr Thr Val Ser Ala Met Ala Cys Val Phe Lys Leu Leu
 305 310 315 320

Ser Ser Asn Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Gly
 325 330 335

Ile Leu Ser Asn Lys Leu Glu Gly Asp Glu Ile Thr Trp Lys Asp Val
 340 345 350

Lys Ser Met Lys Tyr Thr Trp Gln Val Val Gln Glu Thr Leu Arg Leu
 355 360 365

Tyr Pro Ser Ile Phe Gly Ser Phe Arg Gln Ala Ile Thr Asp Ile His
 370 375 380

Tyr Asn Gly Tyr Ile Ile Pro Lys Gly Trp Lys Leu Leu Trp Thr Pro
 385 390 395 400

Tyr Thr Thr His Pro Lys Glu Met Tyr Phe Ser Glu Pro Glu Lys Phe
 405 410 415

Leu Pro Ser Arg Phe Asp Gln Glu Gly Lys Leu Val Ala Pro Tyr Thr
 420 425 430

Phe Leu Pro Phe Gly Gly Gly Gln Arg Ser Cys Pro Gly Trp Glu Phe
 435 440 445

Ser Lys Met Glu Ile Leu Leu Ser Val His His Phe Val Lys Thr Phe
 450 455 460

Ser Thr Phe Thr Pro Val Asp Pro Ala Glu Ile Ile Ala Arg Asp Ser
 465 470 475 480

Leu Cys Pro Leu Pro Ser Asn Gly Phe Ser Val Lys Leu Phe Pro Arg
 485 490 495

Ser Tyr Ser Leu His Thr Gly Asn Gln Val Lys Lys Ile
 500 505

<210> 13
 <211> 1503
 <212> DNA
 <213> *Taxus cuspidata*

<220>
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 <222> (1151)..(1151)
 <223> n is a, c, g, or t

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 ctctggttct tcttccataa aaacgggttc tctgttactc tccccctgg aaatttaggc 180
 ttccctttca ttggggagac cataccattc ttgagggcac ttcgatcaga aacacctcag 240
 acgttttttg atgagagggg gaagaaattc ggtgttgtat tcaagactcg gatagttggg 300
 catcccacag ttgtactctg cgggcctgag ggaaaccgct ttcttctctc caacgaggac 360
 aaactgggtgc aggcgtcatt gcccaactct tccgagaaac taattgggaa atattccatt 420
 ctgtccaaaa gaggggagga gcatcgcata ttacgtgctg cacttgcccg ctttttgcca 480
 cccaagctt tgcaggggta tgttgctaaa atgagttcag aaatccaaca tcatatcaag 540
 caaaaatgga agggaaatga tgaagtgaag gtgcttcctc tgataagaac cctgatcttc 600
 aacattgcaa gcagcctgtt ttctggcata aatgatgaac accaacagga acagcttcat 660
 catcttttgg aagccattgt tctgggaagt ctgtctgttc cgctcgactt tccaggaact 720
 cgttttcgta aagctcttga tgcgcgggtc aagctggatg agattctttc ttctttaatg 780

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gagagcagaa gaagggatct gcgtttgggc acggcttctg agaatcaaga tcttctttct      840
gtgttgctca ccttcaaaga tgaaagaggg aatccactca cagacaagga aatcttcgac      900
aatttttcat ttatgcttca tgcctcgtat gataccactg tttcaccaac gggtttgatg      960
cttaagcttc tcttctctag tcctgattgc tatgaaaaac tagttcaaga acaattggga     1020
atagttggca ataaaaagga gggagaagaa atcagctgga acgatctgaa agctatgaaa     1080
tatacatgca aggttggtgca ggaaagtatg aggatgctcc ctccagtttt tggatcgtat     1140
cgcaaggcta ncacctatat ccattatgat gggatatacaa ttccaaaagg atggaatata     1200
ttctggtcac cttatactac acacgggaaa gaagaatact tcaatgaagc ggacaagttc     1260
atgccttcga gattcgagga aggcaaatat gttgctcctt acacattctt gccattcgga     1320
gcaggtctgc gcgtatgtcc aggatgggaa tttgcaaaga ccgagatatt actgttcgtc     1380
catcatttta ttacaacttt cagcagctac atcccaattg accccaaaga taaaatttca     1440
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taa                                                                    1503

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<210> 14
<211> 502
<212> PRT
<213> Taxus cuspidata

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<220>
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<222> (384)..(384)
<223> Xaa can be any naturally occurring amino acid

<400> 14

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Met Asp Ser Phe Asn Phe Leu Arg Gly Ile Gly Ala Asp Phe Gly Gly
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Phe Ile Gln Phe Gln Ser Ser Pro Ala Val Leu Ser Leu Ser Leu Ile
          20          25          30

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```

Thr Thr Ile Leu Gly Val Leu Leu Leu Trp Phe Phe Leu His Lys Asn
35          40          45

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```

Gly Ser Ser Val Thr Leu Pro Pro Gly Asn Leu Gly Phe Pro Phe Ile
50          55          60

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Gly Glu Thr Ile Pro Phe Leu Arg Ala Leu Arg Ser Glu Thr Pro Gln
65          70          75          80

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Thr Phe Phe Asp Glu Arg Val Lys Lys Phe Gly Val Val Phe Lys Thr
 85 90 95
 Arg Ile Val Gly His Pro Thr Val Val Leu Cys Gly Pro Glu Gly Asn
 100 105 110
 Arg Phe Leu Leu Ser Asn Glu Asp Lys Leu Val Gln Ala Ser Leu Pro
 115 120 125
 Asn Ser Ser Glu Lys Leu Ile Gly Lys Tyr Ser Ile Leu Ser Lys Arg
 130 135 140
 Gly Glu Glu His Arg Ile Leu Arg Ala Ala Leu Ala Arg Phe Leu Arg
 145 150 155 160
 Pro Gln Ala Leu Gln Gly Tyr Val Ala Lys Met Ser Ser Glu Ile Gln
 165 170 175
 His His Ile Lys Gln Lys Trp Lys Gly Asn Asp Glu Val Lys Val Leu
 180 185 190
 Pro Leu Ile Arg Thr Leu Ile Phe Asn Ile Ala Ser Ser Leu Phe Phe
 195 200 205
 Gly Ile Asn Asp Glu His Gln Gln Glu Gln Leu His His Leu Leu Glu
 210 215 220
 Ala Ile Val Leu Gly Ser Leu Ser Val Pro Leu Asp Phe Pro Gly Thr
 225 230 235 240
 Arg Phe Arg Lys Ala Leu Asp Ala Arg Ser Lys Leu Asp Glu Ile Leu
 245 250 255
 Ser Ser Leu Met Glu Ser Arg Arg Arg Asp Leu Arg Leu Gly Thr Ala
 260 265 270
 Ser Glu Asn Gln Asp Leu Leu Ser Val Leu Leu Thr Phe Lys Asp Glu
 275 280 285
 Arg Gly Asn Pro Leu Thr Asp Lys Glu Ile Phe Asp Asn Phe Ser Phe
 290 295 300
 Met Leu His Ala Ser Tyr Asp Thr Thr Val Ser Pro Thr Gly Leu Met
 305 310 315 320
 Leu Lys Leu Leu Phe Ser Ser Pro Asp Cys Tyr Glu Lys Leu Val Gln


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<210> 15
<211> 1494
<212> DNA
<213> Taxus cuspidata

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cgttacaatc accgatcttc tgttaaactt ccccttgga agttaggttt tcctctcatc 180
ggggagacca tacaattatt gcgggacactc cgatcagaaa cacctcaaaa gttttttgat 240

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gatagattga agaaattcgg tcctgtttac atgacttccc taattgggca tcccacagtt 300
gtactctgcg ggcctgcggg aaacaaatta gttctttcga acgaggacaa gctggtagag 360
atggaagggc ccaagtcttt catgaaactg attggggaag attccattgt tgctaaaaga 420
ggcgaggatc atcgcatott acgcactgca cttgctcggg ttttgggcgc tcaagcttta 480
caaaattatc tgggtagaat gagttcagaa ataggacacc atttcaatga aaaatggaag 540
ggtaaagatg aagtgaagggt gcttcctttg gtaagagggc ttatcttctc cattgcaagc 600
accctgtttt tcgatgtaaa tgatggacac caacagaagc aacttcatca tcttctggaa 660
actattcttg tgggaagttt gtcagtcccg ctggactttc caggaactcg ttatcgtaaa 720
gggcttcagg cgcggtgaa gcttgatgaa attctctcct ctctaataaa acgcagaaga 780
agagatctgc gttcaggcat agcttctgat gatcaagatc tactgtcggg gttgctcacc 840
ttcagagatg aaaaagggaa ctactgaca gaccagggga ttctggacaa cttttctgct 900
atgtttcatg cttcatatga caccactggt gcaccaatgg cettgatatt taagcttcta 960
tactccaatc ctgaatacca tgaaaaagta tttcaagagc agttggaaat aattggcaat 1020
aaaaaggaag gggaagaaat cagttggaag gatttgaaat ctatgaaata tacatggcaa 1080
gcagttcaag aatcactacg aatgtaccca ccagtttttg gaatatttcg taaggctatc 1140
actgatattc attatgatgg gtatacaatt ccaaaaggat ggagggtttt atgttcacct 1200
tatactacac atctgagaga agagtacttc cctgagcctg aagaattcag gccttcaaga 1260
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cgcacatgtc caggatggga attttcaaag attgaaatat tactgtttgt ccatcatttc 1380
gttaaaaatt tcagcagcta cattccagtt gatcccaatg aaaaagtfff atcagatcca 1440
ctacctcctc tcctgccaa tggattttcc ataaaacttt ttccgagatc ctaa 1494

<210> 16

<211> 497

<212> PRT

<213> *Taxus cuspidata*

<400> 16

Met Asp Ser Phe Ile Phe Leu Arg Ser Ile Gly Thr Lys Phe Gly Gln
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Leu Glu Ser Ser Pro Ala Ile Leu Ser Leu Thr Leu Ala Pro Ile Leu
20 25 30

Ala Ile Ile Leu Leu Leu Leu Phe Arg Tyr Asn His Arg Ser Ser Val
35 40 45

Lys Leu Pro Pro Gly Lys Leu Gly Phe Pro Leu Ile Gly Glu Thr Ile
 50 55 60

Gln Leu Leu Arg Thr Leu Arg Ser Glu Thr Pro Gln Lys Phe Phe Asp
 65 70 75 80

Asp Arg Leu Lys Lys Phe Gly Pro Val Tyr Met Thr Ser Leu Ile Gly
 85 90 95

His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Lys Leu Val Leu
 100 105 110

Ser Asn Glu Asp Lys Leu Val Glu Met Glu Gly Pro Lys Ser Phe Met
 115 120 125

Lys Leu Ile Gly Glu Asp Ser Ile Val Ala Lys Arg Gly Glu Asp His
 130 135 140

Arg Ile Leu Arg Thr Ala Leu Ala Arg Phe Leu Gly Ala Gln Ala Leu
 145 150 155 160

Gln Asn Tyr Leu Gly Arg Met Ser Ser Glu Ile Gly His His Phe Asn
 165 170 175

Glu Lys Trp Lys Gly Lys Asp Glu Val Lys Val Leu Pro Leu Val Arg
 180 185 190

Gly Leu Ile Phe Ser Ile Ala Ser Thr Leu Phe Phe Asp Val Asn Asp
 195 200 205

Gly His Gln Gln Lys Gln Leu His His Leu Leu Glu Thr Ile Leu Val
 210 215 220

Gly Ser Leu Ser Val Pro Leu Asp Phe Pro Gly Thr Arg Tyr Arg Lys
 225 230 235 240

Gly Leu Gln Ala Arg Leu Lys Leu Asp Glu Ile Leu Ser Ser Leu Ile
 245 250 255

Lys Arg Arg Arg Arg Asp Leu Arg Ser Gly Ile Ala Ser Asp Asp Gln
 260 265 270

Asp Leu Leu Ser Val Leu Leu Thr Phe Arg Asp Glu Lys Gly Asn Ser
 275 280 285

Leu Thr Asp Gln Gly Ile Leu Asp Asn Phe Ser Ala Met Phe His Ala
 290 295 300

Ser Tyr Asp Thr Thr Val Ala Pro Met Ala Leu Ile Phe Lys Leu Leu
 305 310 315 320

Tyr Ser Asn Pro Glu Tyr His Glu Lys Val Phe Gln Glu Gln Leu Glu
 325 330 335

Ile Ile Gly Asn Lys Lys Glu Gly Glu Glu Ile Ser Trp Lys Asp Leu
 340 345 350

Lys Ser Met Lys Tyr Thr Trp Gln Ala Val Gln Glu Ser Leu Arg Met
 355 360 365

Tyr Pro Pro Val Phe Gly Ile Phe Arg Lys Ala Ile Thr Asp Ile His
 370 375 380

Tyr Asp Gly Tyr Thr Ile Pro Lys Gly Trp Arg Val Leu Cys Ser Pro
 385 390 395 400

Tyr Thr Thr His Leu Arg Glu Glu Tyr Phe Pro Glu Pro Glu Glu Phe
 405 410 415

Arg Pro Ser Arg Phe Glu Asp Glu Gly Arg His Val Thr Pro Tyr Thr
 420 425 430

Tyr Val Pro Phe Gly Gly Gly Leu Arg Thr Cys Pro Gly Trp Glu Phe
 435 440 445

Ser Lys Ile Glu Ile Leu Leu Phe Val His His Phe Val Lys Asn Phe
 450 455 460

Ser Ser Tyr Ile Pro Val Asp Pro Asn Glu Lys Val Leu Ser Asp Pro
 465 470 475 480

Leu Pro Pro Leu Pro Ala Asn Gly Phe Ser Ile Lys Leu Phe Pro Arg
 485 490 495

Ser

<210> 17

<211> 1458

<212> DNA

<213> Taxus cuspidata

<400> 17

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ggaaatctag gcttcctctt gggtggggag aactgcagtc tcgtgaggtc acttggtctg      180
agcactccac agcagtttat tgaagagaga atgagcaaatt ttggggatgt gttcaagact      240
tccataatcg ggcacccac agtagtgctg tgtggacctg ccggaaccg gttggttctg      300
tcgaacgaga acaagctggg gcagatgtca tggccgagct ccatgatgaa actcatcggc      360
gaagattgtc tcggcggcaa aacgggagag cagcatcgga tcgtacgcgc tgcactaact      420
cggtttttgg gtctcaagc attgcagaat catttcgcta aaatgagctc gggaatccaa      480
cgccacatca atgaaaaatg gaagggaag gatgaggcca ctgtacttcc tttggtaaaa      540
gacctcgtct tctccgtcgc aagccgcttg ttttttggtg taactgagga gcacctgcag      600
gagcaacttc ataacttggt ggaagttatt cttgtgggat ctttttctgt tccactcaac      660
attcccggat tcagttacca taaagcgatt caggcaaggg ccaccctcgc tgacatcatg      720
accatttga tagaaaagag gagaaatgag ctgcgtgcag gcaactgcac tgagaatcaa      780
gatttgcctc ctgttttgc cactttcact gacgaaaggg ggaattcact ggcggacaag      840
gagatcctcg acaacttttc tatgttactt catggatcat atgactccac caattcccca      900
cttaccatgt tgattaaagt cttggcctcc catccagaaa gctatgaaaa agtgggtcaa      960
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aaggagatga aatattcatg gcaagttggt caggaaacat tgcgcagtga tcctccatt     1080
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ggatggaaac ttttatggac aacttacagt actcaaacca aggaagagta tttcaaggac     1200
gccgatcaat tcaagccatc aagatttgag gaggaaggga agcatgtaac cccttacaca     1260
tacttacctt tcggaggagg catgcgtggt tgtccagggt gggaattcgc caagatggag     1320
acattactgt ttctccatca ttttggttaa gccttctctg ggttgaaggc aattgatcca     1380
aatgaaaaac tttcagggaa accacttcct cctctccctg tcaatgggct tcccattaaa     1440
ctctattcca gatcttaa                                     1458

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<210> 18

<211> 485

<212> PRT

<213> *Taxus cuspidata*

<400> 18

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Met Asp Ala Leu Lys Gln Leu Glu Val Ser Pro Ser Ile Leu Phe Val
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Thr Leu Ala Val Met Ala Gly Ile Ile Leu Phe Phe Arg Ser Lys Arg
 20 25 30

His Ser Ser Val Lys Leu Pro Pro Gly Asn Leu Gly Phe Pro Leu Val
 35 40 45

Gly Glu Thr Leu Gln Phe Val Arg Ser Leu Gly Ser Ser Thr Pro Gln
 50 55 60

Gln Phe Ile Glu Glu Arg Met Ser Lys Phe Gly Asp Val Phe Lys Thr
 65 70 75 80

Ser Ile Ile Gly His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn
 85 90 95

Arg Leu Val Leu Ser Asn Glu Asn Lys Leu Val Gln Met Ser Trp Pro
 100 105 110

Ser Ser Met Met Lys Leu Ile Gly Glu Asp Cys Leu Gly Gly Lys Thr
 115 120 125

Gly Glu Gln His Arg Ile Val Arg Ala Ala Leu Thr Arg Phe Leu Gly
 130 135 140

Pro Gln Ala Leu Gln Asn His Phe Ala Lys Met Ser Ser Gly Ile Gln
 145 150 155 160

Arg His Ile Asn Glu Lys Trp Lys Gly Lys Asp Glu Ala Thr Val Leu
 165 170 175

Pro Leu Val Lys Asp Leu Val Phe Ser Val Ala Ser Arg Leu Phe Phe
 180 185 190

Gly Ile Thr Glu Glu His Leu Gln Glu Gln Leu His Asn Leu Leu Glu
 195 200 205

Val Ile Leu Val Gly Ser Phe Ser Val Pro Leu Asn Ile Pro Gly Phe
 210 215 220

Ser Tyr His Lys Ala Ile Gln Ala Arg Ala Thr Leu Ala Asp Ile Met
 225 230 235 240

Thr His Leu Ile Glu Lys Arg Arg Asn Glu Leu Arg Ala Gly Thr Ala
 245 250 255

Ser Glu Asn Gln Asp Leu Leu Ser Val Leu Leu Thr Phe Thr Asp Glu
 260 265 270

Arg Gly Asn Ser Leu Ala Asp Lys Glu Ile Leu Asp Asn Phe Ser Met
 275 280 285

Leu Leu His Gly Ser Tyr Asp Ser Thr Asn Ser Pro Leu Thr Met Leu
 290 295 300

Ile Lys Val Leu Ala Ser His Pro Glu Ser Tyr Glu Lys Val Ala Gln
 305 310 315 320

Glu Gln Phe Gly Ile Leu Ser Thr Lys Met Glu Gly Glu Glu Ile Ala
 325 330 335

Trp Lys Asp Leu Lys Glu Met Lys Tyr Ser Trp Gln Val Val Gln Glu
 340 345 350

Thr Leu Arg Met Tyr Pro Pro Ile Phe Gly Thr Phe Arg Lys Ala Ile
 355 360 365

Thr Asp Ile His Tyr Asn Gly Tyr Thr Ile Pro Lys Gly Trp Lys Leu
 370 375 380

Leu Trp Thr Thr Tyr Ser Thr Gln Thr Lys Glu Glu Tyr Phe Lys Asp
 385 390 395 400

Ala Asp Gln Phe Lys Pro Ser Arg Phe Glu Glu Glu Gly Lys His Val
 405 410 415

Thr Pro Tyr Thr Tyr Leu Pro Phe Gly Gly Gly Met Arg Val Cys Pro
 420 425 430

Gly Trp Glu Phe Ala Lys Met Glu Thr Leu Leu Phe Leu His His Phe
 435 440 445

Val Lys Ala Phe Ser Gly Leu Lys Ala Ile Asp Pro Asn Glu Lys Leu
 450 455 460

Ser Gly Lys Pro Leu Pro Pro Leu Pro Val Asn Gly Leu Pro Ile Lys
 465 470 475 480

Leu Tyr Ser Arg Ser
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<210> 19
<211> 2700
<212> DNA
<213> Taxus brevifolia
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<220>
<221> CDS
<222> (22) .. (2610)
<223> coding sequence
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Trp	Lys	Thr	Gly	His	Ser	Gln	Val	Gln	Gln	Gly	Ala	Glu	Phe	Ile	Ala		
		205					210				215						
gag	aat	cta	aga	tta	ctc	aat	gag	gaa	gat	gag	ttg	tcc	ccg	gat	ttc		723
Glu	Asn	Leu	Arg	Leu	Leu	Asn	Glu	Glu	Asp	Glu	Leu	Ser	Pro	Asp	Phe		
	220					225				230							
caa	ata	atc	ttt	cct	gct	ctg	ctg	caa	aag	gca	aaa	gcg	ttg	ggg	atc		771
Gln	Ile	Ile	Phe	Pro	Ala	Leu	Leu	Gln	Lys	Ala	Lys	Ala	Leu	Gly	Ile		
235					240					245					250		
aat	ctt	cct	tac	gat	ctt	cca	ttt	atc	aaa	tat	ttg	tcg	aca	aca	cgg		819
Asn	Leu	Pro	Tyr	Asp	Leu	Pro	Phe	Ile	Lys	Tyr	Leu	Ser	Thr	Thr	Arg		
			255						260					265			
gaa	gcc	agg	ctt	aca	gat	gtt	tct	gcg	gca	gca	gac	aat	att	cca	gcc		867
Glu	Ala	Arg	Leu	Thr	Asp	Val	Ser	Ala	Ala	Ala	Asp	Asn	Ile	Pro	Ala		
			270					275					280				
aac	atg	ttg	aat	gcg	ttg	gaa	ggg	ctc	gag	gaa	gtt	att	gac	tgg	aac		915
Asn	Met	Leu	Asn	Ala	Leu	Glu	Gly	Leu	Glu	Glu	Val	Ile	Asp	Trp	Asn		
		285					290					295					
aag	att	atg	agg	ttt	caa	agt	aaa	gat	gga	tct	ttc	ctg	agc	tcc	cct		963
Lys	Ile	Met	Arg	Phe	Gln	Ser	Lys	Asp	Gly	Ser	Phe	Leu	Ser	Ser	Pro		
	300					305					310						
gcc	tcc	act	gcc	tgt	gta	ctg	atg	aat	aca	ggg	gac	gaa	aaa	tgt	ttc		1011
Ala	Ser	Thr	Ala	Cys	Val	Leu	Met	Asn	Thr	Gly	Asp	Glu	Lys	Cys	Phe		
315					320					325					330		
act	ttt	ctc	aac	aat	ctg	ctc	gac	aaa	ttc	ggc	ggc	tgc	gtg	ccc	tgt		1059
Thr	Phe	Leu	Asn	Asn	Leu	Leu	Asp	Lys	Phe	Gly	Gly	Cys	Val	Pro	Cys		
			335					340						345			
atg	tat	tcc	atc	gat	ctg	ctg	gaa	cgc	ctt	tcg	ctg	gtt	gat	aac	att		1107
Met	Tyr	Ser	Ile	Asp	Leu	Leu	Glu	Arg	Leu	Ser	Leu	Val	Asp	Asn	Ile		
			350					355					360				
gag	cat	ctc	gga	atc	ggg	cgc	cat	ttc	aaa	caa	gaa	atc	aaa	gga	gct		1155
Glu	His	Leu	Gly	Ile	Gly	Arg	His	Phe	Lys	Gln	Glu	Ile	Lys	Gly	Ala		
		365				370						375					
ctt	gat	tat	gtc	tac	aga	cat	tgg	agt	gaa	agg	ggc	atc	ggg	tgg	ggc		1203
Leu	Asp	Tyr	Val	Tyr	Arg	His	Trp	Ser	Glu	Arg	Gly	Ile	Gly	Trp	Gly		
	380					385					390						
aga	gac	agc	ctt	gtt	cca	gat	ctc	aac	acc	aca	gcc	ctc	ggc	ctg	cga		1251
Arg	Asp	Ser	Leu	Val	Pro	Asp	Leu	Asn	Thr	Thr	Ala	Leu	Gly	Leu	Arg		
395					400					405					410		
act	ctt	cgc	atg	cac	gga	tac	aat	gtt	tct	tca	gac	gtt	ttg	aat	aat		1299
Thr	Leu	Arg	Met	His	Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Asn	Asn		
				415				420						425			
ttc	aaa	gat	gaa	aac	ggg	cgg	ttc	ttc	tcc	tct	gcg	ggc	caa	acc	cat		1347
Phe	Lys	Asp	Glu	Asn	Gly	Arg	Phe	Phe	Ser	Ser	Ala	Gly	Gln	Thr	His		

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gtc	gaa	ttg	aga	agc	gtg	gtg	aat	ctt	ttc	aga	gct	tcc	gac	ctt	gca	1395
Val	Glu	Leu	Arg	Ser	Val	Val	Asn	Leu	Phe	Arg	Ala	Ser	Asp	Leu	Ala	
		445					450					455				
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Phe	Pro	Asp	Glu	Arg	Ala	Met	Asp	Asp	Ala	Arg	Lys	Phe	Ala	Glu	Pro	
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tat	ctt	aga	gag	gca	ctt	gca	acg	aaa	atc	tca	acc	aat	aca	aaa	cta	1491
Tyr	Leu	Arg	Glu	Ala	Leu	Ala	Thr	Lys	Ile	Ser	Thr	Asn	Thr	Lys	Leu	
475					480					485					490	
ttc	aaa	gag	att	gag	tac	gtg	gtg	gag	tac	cct	tgg	cac	atg	agt	atc	1539
Phe	Lys	Glu	Ile	Glu	Tyr	Val	Val	Glu	Tyr	Pro	Trp	His	Met	Ser	Ile	
				495				500						505		
cca	cgc	tta	gaa	gcc	aga	agt	tat	att	gat	tca	tat	gac	gac	aat	tat	1587
Pro	Arg	Leu	Glu	Ala	Arg	Ser	Tyr	Ile	Asp	Ser	Tyr	Asp	Asp	Asn	Tyr	
		510					515						520			
gta	tgg	cag	agg	aag	act	cta	tat	aga	atg	cca	tct	ttg	agt	aat	tca	1635
Val	Trp	Gln	Arg	Lys	Thr	Leu	Tyr	Arg	Met	Pro	Ser	Leu	Ser	Asn	Ser	
		525					530					535				
aaa	tgt	tta	gaa	ttg	gca	aaa	ttg	gac	ttc	aat	atc	gta	caa	tct	ttg	1683
Lys	Cys	Leu	Glu	Leu	Ala	Lys	Leu	Asp	Phe	Asn	Ile	Val	Gln	Ser	Leu	
	540					545					550					
cat	caa	gag	gag	ttg	aag	ctt	cta	aca	aga	tgg	tgg	aag	gaa	tcc	ggc	1731
His	Gln	Glu	Glu	Leu	Lys	Leu	Leu	Thr	Arg	Trp	Trp	Lys	Glu	Ser	Gly	
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Met	Ala	Asp	Ile	Asn	Phe	Thr	Arg	His	Arg	Val	Ala	Glu	Val	Tyr	Phe	
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tca	tca	gct	aca	ttt	gaa	ccc	gaa	tat	tct	gcc	act	aga	att	gcc	ttc	1827
Ser	Ser	Ala	Thr	Phe	Glu	Pro	Glu	Tyr	Ser	Ala	Thr	Arg	Ile	Ala	Phe	
			590					595					600			
aca	aaa	att	ggt	tgt	tta	caa	gtc	ctt	ttt	gat	gat	atg	gct	gac	atc	1875
Thr	Lys	Ile	Gly	Cys	Leu	Gln	Val	Leu	Phe	Asp	Asp	Met	Ala	Asp	Ile	
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Trp	Asp	Thr	Ser	Leu	Leu	His	Glu	Ile	Pro	Glu	Cys	Met	Gln	Thr	Cys	
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ttt	aaa	gtt	tgg	ttc	aaa	tta	atg	gaa	gaa	gta	aat	aat	gat	gtg	gtt	2019
Phe	Lys	Val	Trp	Phe	Lys	Leu	Met	Glu	Glu	Val	Asn	Asn	Asp	Val	Val	
				655					660					665		
aag	gta	caa	gga	cgt	gac	atg	ctc	gct	cac	ata	aga	aaa	ccc	tgg	gag	2067
Lys	Val	Gln	Gly	Arg	Asp	Met	Leu	Ala	His	Ile	Arg	Lys	Pro	Trp	Glu	
			670					675					680			

ttg tac ttc aat tgt tat gta caa gaa agg gag tgg ctt gaa gcc ggg 2115
 Leu Tyr Phe Asn Cys Tyr Val Gln Glu Arg Glu Trp Leu Glu Ala Gly
 685 690 695

tat ata cca act ttt gaa gag tac tta aag act tat gct ata tca gta 2163
 Tyr Ile Pro Thr Phe Glu Tyr Leu Lys Thr Tyr Ala Ile Ser Val
 700 705 710

ggc ctt gga ccg tgt acc cta caa cca ata cta cta atg ggt gag ctt 2211
 Gly Leu Gly Pro Cys Thr Leu Gln Pro Ile Leu Leu Met Gly Glu Leu
 715 720 725 730

gtg aaa gat gat gtt gtt gag aaa gtg cac tat ccc tca aat atg ttt 2259
 Val Lys Asp Asp Val Val Glu Lys Val His Tyr Pro Ser Asn Met Phe
 735 740 745

gag ctt gta tcc ttg agc tgg cga cta aca aac gac acc aaa aca tat 2307
 Glu Leu Val Ser Leu Ser Trp Arg Leu Thr Asn Asp Thr Lys Thr Tyr
 750 755 760

cag gct gaa aag gct cga gga caa caa gcc tca ggc ata gca tgc tat 2355
 Gln Ala Glu Lys Ala Arg Gly Gln Gln Ala Ser Gly Ile Ala Cys Tyr
 765 770 775

atg aag gat aat cca gga gca act gag gaa gat gcc att aag cac ata 2403
 Met Lys Asp Asn Pro Gly Ala Thr Glu Glu Asp Ala Ile Lys His Ile
 780 785 790

tgt cgt gtt gtt gat cgg gcc ttg aaa gaa gca agc ttt gaa tat ttc 2451
 Cys Arg Val Val Asp Arg Ala Leu Lys Glu Ala Ser Phe Glu Tyr Phe
 795 800 805 810

aaa cca tcc aat gat atc cca atg ggt tgc aag tcc ttt att ttt aac 2499
 Lys Pro Ser Asn Asp Ile Pro Met Gly Cys Lys Ser Phe Ile Phe Asn
 815 820 825

ctt aga ttg tgt gtc caa atc ttt tac aag ttt ata gat ggg tac gga 2547
 Leu Arg Leu Cys Val Gln Ile Phe Tyr Lys Phe Ile Asp Gly Tyr Gly
 830 835 840

atc gcc aat gag gag att aag gac tat ata aga aaa gtt tat att gat 2595
 Ile Ala Asn Glu Glu Ile Lys Asp Tyr Ile Arg Lys Val Tyr Ile Asp
 845 850 855

cca att caa gta tga tatatcatgt aaaacctctt tttcatgata aattgactta 2650
 Pro Ile Gln Val
 860

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<211> 862

<212> PRT

<213> Taxus brevifolia

<400> 20

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Asn Lys Ala Ile His Asp Pro Thr Asn Cys Arg Ala Lys Ser Glu Arg
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 Gln Met Met Trp Val Cys Ser Arg Ser Gly Arg Thr Arg Val Lys Met
 35 40 45
 Ser Arg Gly Ser Gly Gly Pro Gly Pro Val Val Met Met Ser Ser Ser
 50 55 60
 Thr Gly Thr Ser Lys Val Val Ser Glu Thr Ser Ser Thr Ile Val Asp
 65 70 75 80
 Asp Ile Pro Arg Leu Ser Ala Asn Tyr His Gly Asp Leu Trp His His
 85 90 95
 Asn Val Ile Gln Thr Leu Glu Thr Pro Phe Arg Glu Ser Ser Thr Tyr
 100 105 110
 Gln Glu Arg Ala Asp Glu Leu Val Val Lys Ile Lys Asp Met Phe Asn
 115 120 125
 Ala Leu Gly Asp Gly Asp Ile Ser Pro Ser Ala Tyr Asp Thr Ala Trp
 130 135 140
 Val Ala Arg Leu Ala Thr Ile Ser Ser Asp Gly Ser Glu Lys Pro Arg
 145 150 155 160
 Phe Pro Gln Ala Leu Asn Trp Val Phe Asn Asn Gln Leu Gln Asp Gly
 165 170 175
 Ser Trp Gly Ile Glu Ser His Phe Ser Leu Cys Asp Arg Leu Leu Asn
 180 185 190
 Thr Thr Asn Ser Val Ile Ala Leu Ser Val Trp Lys Thr Gly His Ser
 195 200 205
 Gln Val Gln Gln Gly Ala Glu Phe Ile Ala Glu Asn Leu Arg Leu Leu
 210 215 220
 Asn Glu Glu Asp Glu Leu Ser Pro Asp Phe Gln Ile Ile Phe Pro Ala
 225 230 235 240
 Leu Leu Gln Lys Ala Lys Ala Leu Gly Ile Asn Leu Pro Tyr Asp Leu
 245 250 255

Pro Phe Ile Lys Tyr Leu Ser Thr Thr Arg Glu Ala Arg Leu Thr Asp
 260 265 270

Val Ser Ala Ala Ala Asp Asn Ile Pro Ala Asn Met Leu Asn Ala Leu
 275 280 285

Glu Gly Leu Glu Glu Val Ile Asp Trp Asn Lys Ile Met Arg Phe Gln
 290 295 300

Ser Lys Asp Gly Ser Phe Leu Ser Ser Pro Ala Ser Thr Ala Cys Val
 305 310 315 320

Leu Met Asn Thr Gly Asp Glu Lys Cys Phe Thr Phe Leu Asn Asn Leu
 325 330 335

Leu Asp Lys Phe Gly Gly Cys Val Pro Cys Met Tyr Ser Ile Asp Leu
 340 345 350

Leu Glu Arg Leu Ser Leu Val Asp Asn Ile Glu His Leu Gly Ile Gly
 355 360 365

Arg His Phe Lys Gln Glu Ile Lys Gly Ala Leu Asp Tyr Val Tyr Arg
 370 375 380

His Trp Ser Glu Arg Gly Ile Gly Trp Gly Arg Asp Ser Leu Val Pro
 385 390 395 400

Asp Leu Asn Thr Thr Ala Leu Gly Leu Arg Thr Leu Arg Met His Gly
 405 410 415

Tyr Asn Val Ser Ser Asp Val Leu Asn Asn Phe Lys Asp Glu Asn Gly
 420 425 430

Arg Phe Phe Ser Ser Ala Gly Gln Thr His Val Glu Leu Arg Ser Val
 435 440 445

Val Asn Leu Phe Arg Ala Ser Asp Leu Ala Phe Pro Asp Glu Arg Ala
 450 455 460

Met Asp Asp Ala Arg Lys Phe Ala Glu Pro Tyr Leu Arg Glu Ala Leu
 465 470 475 480

Ala Thr Lys Ile Ser Thr Asn Thr Lys Leu Phe Lys Glu Ile Glu Tyr
 485 490 495

Val Val Glu Tyr Pro Trp His Met Ser Ile Pro Arg Leu Glu Ala Arg
 500 505 510

Ser Tyr Ile Asp Ser Tyr Asp Asp Asn Tyr Val Trp Gln Arg Lys Thr
 515 520 525

Leu Tyr Arg Met Pro Ser Leu Ser Asn Ser Lys Cys Leu Glu Leu Ala
 530 535 540

Lys Leu Asp Phe Asn Ile Val Gln Ser Leu His Gln Glu Glu Leu Lys
 545 550 555 560

Leu Leu Thr Arg Trp Trp Lys Glu Ser Gly Met Ala Asp Ile Asn Phe
 565 570 575

Thr Arg His Arg Val Ala Glu Val Tyr Phe Ser Ser Ala Thr Phe Glu
 580 585 590

Pro Glu Tyr Ser Ala Thr Arg Ile Ala Phe Thr Lys Ile Gly Cys Leu
 595 600 605

Gln Val Leu Phe Asp Asp Met Ala Asp Ile Phe Ala Thr Leu Asp Glu
 610 615 620

Leu Lys Ser Phe Thr Glu Gly Val Lys Arg Trp Asp Thr Ser Leu Leu
 625 630 635 640

His Glu Ile Pro Glu Cys Met Gln Thr Cys Phe Lys Val Trp Phe Lys
 645 650 655

Leu Met Glu Glu Val Asn Asn Asp Val Val Lys Val Gln Gly Arg Asp
 660 665 670

Met Leu Ala His Ile Arg Lys Pro Trp Glu Leu Tyr Phe Asn Cys Tyr
 675 680 685

Val Gln Glu Arg Glu Trp Leu Glu Ala Gly Tyr Ile Pro Thr Phe Glu
 690 695 700

Glu Tyr Leu Lys Thr Tyr Ala Ile Ser Val Gly Leu Gly Pro Cys Thr
 705 710 715 720

Leu Gln Pro Ile Leu Leu Met Gly Glu Leu Val Lys Asp Asp Val Val
 725 730 735

Glu Lys Val His Tyr Pro Ser Asn Met Phe Glu Leu Val Ser Leu Ser

740 745 750
 Trp Arg Leu Thr Asn Asp Thr Lys Thr Tyr Gln Ala Glu Lys Ala Arg
 755 760 765
 Gly Gln Gln Ala Ser Gly Ile Ala Cys Tyr Met Lys Asp Asn Pro Gly
 770 775 780
 Ala Thr Glu Glu Asp Ala Ile Lys His Ile Cys Arg Val Val Asp Arg
 785 790 795 800
 Ala Leu Lys Glu Ala Ser Phe Glu Tyr Phe Lys Pro Ser Asn Asp Ile
 805 810 815
 Pro Met Gly Cys Lys Ser Phe Ile Phe Asn Leu Arg Leu Cys Val Gln
 820 825 830
 Ile Phe Tyr Lys Phe Ile Asp Gly Tyr Gly Ile Ala Asn Glu Glu Ile
 835 840 845
 Lys Asp Tyr Ile Arg Lys Val Tyr Ile Asp Pro Ile Gln Val
 850 855 860

<210> 21
 <211> 1419
 <212> DNA
 <213> *Taxus cuspidata*

<220>
 <221> CDS
 <222> (11)..(1330)
 <223> coding sequence

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 Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys
 1 5 10
 gtg atg gtt ggg cca tcc ccg cct ctg ccc aaa acc acc ctg caa ctc 97
 Val Met Val Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu
 15 20 25
 tcc tcc ata gac aac ctg cca ggg gta aga gga agc att ttc aat gcc 145
 Ser Ser Ile Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala
 30 35 40 45
 ttg tta att tac aat gcc tct ccc tct ccc acc atg atc tct gca gat 193
 Leu Leu Ile Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp
 50 55 60
 cct gca aaa cca att aga gaa gct ctc gcc aag atc ctg gtt tat tat 241
 Pro Ala Lys Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr

65	70	75	
ccc cct ttt gct ggg cgc ctc aga gag aca gaa aat ggg gat ctg gaa Pro Pro Phe Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu 80 85 90			289
gtg gaa tgc aca ggg gag ggt gct atg ttt ttg gaa gcc atg gca gac Val Glu Cys Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp 95 100 105			337
aat gag ctg tct gtg ttg gga gat ttt gat gac agc aat cca tca ttt Asn Glu Leu Ser Val Leu Gly Asp Phe Asp Ser Asn Pro Ser Phe 110 115 120 125			385
cag cag cta ctt ttt tgc ctt cca ctc gat acc aat ttc aaa gac ctc Gln Gln Leu Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu 130 135 140			433
tct ctt ctg gtt gtt cag gta act cgt ttt aca tgt gga ggc ttt gtt Ser Leu Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val 145 150 155			481
gtt gga gtg agt ttc cac cat ggt gta tgt gat ggt cga gga gcg gcc Val Gly Val Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala 160 165 170			529
caa ttt ctt aaa ggt ttg gca gag atg gca cgg gga gag gtt aag ctc Gln Phe Leu Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu 175 180 185			577
tca ttg gaa cca ata tgg aat agg gaa cta gtg aag ctt gat gac cct Ser Leu Glu Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro 190 195 200 205			625
aaa tac ctt caa ttt ttt cac ttt gaa ttc cta cga gcg cct tca att Lys Tyr Leu Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile 210 215 220			673
gtt gag aaa att gtt caa aca tat ttt att ata gat ttt gag acc ata Val Glu Lys Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile 225 230 235			721
aat tat atc aaa caa tct gtt atg gaa gaa tgt aaa gaa ttt tgc tct Asn Tyr Ile Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser 240 245 250			769
tca ttc gaa gtt gca tca gca atg act tgg ata gca agg aca aga gct Ser Phe Glu Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala 255 260 265			817
ttt caa att cca gaa agt gag tac gtg aaa att ctc ttc gga atg gac Phe Gln Ile Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp 270 275 280 285			865
atg agg aac tca ttt aat ccc cct ctt cca agc gga tac tat ggt aac Met Arg Asn Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn 290 295 300			913
tcc att ggt acc gca tgt gca gtg gat aat gtt caa gac ctc tta agt Ser Ile Gly Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser 305 310 315			961

gga tct ctt ttg cgt gct ata atg att ata aag aaa tca aag gtc tct 1009
 Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser
 320 325 330
 tta aat gat aat ttc aag tca aga gct gtg gtg aag cca tct gaa ttg 1057
 Leu Asn Asp Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu
 335 340 345
 gat gtg aat atg aat cat gaa aac gta gtt gca ttt gct gat tgg agc 1105
 Asp Val Asn Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser
 350 355 360 365
 cga ttg gga ttt gat gaa gtg gat ttt ggt tgg ggg aat gcg gtg agt 1153
 Arg Leu Gly Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser
 370 375 380
 gta agc cct gtg caa caa cag tct gcg tta gca atg caa aat tat ttt 1201
 Val Ser Pro Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe
 385 390 395
 ctt ttc cta aaa cct tcc aag aac aag ccc gat gga atc aaa ata tta 1249
 Leu Phe Leu Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu
 400 405 410
 atg ttt ctg ccc cta tca aaa atg aag tca ttc aaa att gaa atg gaa 1297
 Met Phe Leu Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu
 415 420 425
 gcc atg atg aaa aaa tat gtg gct aaa gta tga aagtgcaacg atggaaggct 1350
 Ala Met Met Lys Lys Tyr Val Ala Lys Val
 430 435
 tgtatttttg aaataatatt tcaaataatc tcgtggttca aatactttgt taaaaaaaaa 1410
 aaaaaaaaaa 1419

<210> 22
 <211> 439
 <212> PRT
 <213> Taxus cuspidata

<400> 22

Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys Val Met Val
1 5 10 15

Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu Ser Ser Ile
20 25 30

Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala Leu Leu Ile
35 40 45

Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp Pro Ala Lys
50 55 60

Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr Pro Pro Phe
65 70 75 80

Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu Val Glu Cys
85 90 95

Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp Asn Glu Leu
100 105 110

Ser Val Leu Gly Asp Phe Asp Asp Ser Asn Pro Ser Phe Gln Gln Leu
115 120 125

Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu Ser Leu Leu
130 135 140

Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val
145 150 155 160

Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Leu
165 170 175

Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu Ser Leu Glu
180 185 190

Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro Lys Tyr Leu
195 200 205

Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile Val Glu Lys
210 215 220

Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile Asn Tyr Ile
225 230 235 240

Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser Ser Phe Glu
245 250 255

Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala Phe Gln Ile
260 265 270

Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp Met Arg Asn
275 280 285

Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn Ser Ile Gly
290 295 300

Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser Gly Ser Leu

305 310 315 320
 Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser Leu Asn Asp
 325 330 335
 Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu Asp Val Asn
 340 345 350
 Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser Arg Leu Gly
 355 360 365
 Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser Val Ser Pro
 370 375 380
 Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu
 385 390 395 400
 Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu Met Phe Leu
 405 410 415
 Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu Ala Met Met
 420 425 430
 Lys Lys Tyr Val Ala Lys Val
 435

<210> 23
 <211> 1388
 <212> DNA
 <213> *Taxus cuspidata*

<220>
 <221> CDS
 <222> (22)..(1344)
 <223> coding sequence

<400> 23
 aggagagtcc aaatatctac a atg ggc agg ttc aat gta gat atg att gag 51
 Met Gly Arg Phe Asn Val Asp Met Ile Glu
 1 5 10
 cga gtg atc gtg gcg cca tgc ctt caa tcg ccc aaa aat atc ctg cac 99
 Arg Val Ile Val Ala Pro Cys Leu Gln Ser Pro Lys Asn Ile Leu His
 15 20 25
 ctc tcc ccc att gac aac aaa act aga gga cta acc aac ata tta tca 147
 Leu Ser Pro Ile Asp Asn Lys Thr Arg Gly Leu Thr Asn Ile Leu Ser
 30 35 40
 gtc tac aat gcc tcc cag aga gtt tct gtt tct gca gat cct gca aaa 195
 Val Tyr Asn Ala Ser Gln Arg Val Ser Val Ser Ala Asp Pro Ala Lys

45	50	55	
aca att cga gag gct ctc tcc aag gtg ctg gtt tat tat ccc cct ttt Thr Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Pro Pro Phe 60 65 70			243
gct gga agg ctg aga aac aca gaa aat ggg gat ctt gaa gtg gag tgc Ala Gly Arg Leu Arg Asn Thr Glu Asn Gly Asp Leu Glu Val Glu Cys 75 80 85 90			291
aca ggg gag ggt gcc gtc ttt gtg gaa gcc atg gcg gac aac gac ctt Thr Gly Glu Gly Ala Val Phe Val Glu Ala Met Ala Asp Asn Asp Leu 95 100 105			339
tca gta tta caa gat ttc aat gag tac gat cca tca ttt cag cag cta Ser Val Leu Gln Asp Phe Asn Glu Tyr Asp Pro Ser Phe Gln Gln Leu 110 115 120			387
gtt ttt aat ctt cga gag gat gtc aat att gag gac ctc cat ctt cta Val Phe Asn Leu Arg Glu Asp Val Asn Ile Glu Asp Leu His Leu Leu 125 130 135			435
act gtt cag gta act cgt ttt aca tgt gga gga ttt gtt gtg ggc aca Thr Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Thr 140 145 150			483
aga ttc cac cat agt gta tct gat gga aaa gga atc ggc cag tta ctt Arg Phe His His Ser Val Ser Asp Gly Lys Gly Ile Gly Gln Leu Leu 155 160 165 170			531
aaa ggc atg gga gag atg gca agg ggg gag ttt aag ccc tcg tta gaa Lys Gly Met Gly Glu Met Ala Arg Gly Glu Phe Lys Pro Ser Leu Glu 175 180 185			579
cca ata tgg aat aga gaa atg gtg aag cct gaa gac att atg tac ctc Pro Ile Trp Asn Arg Glu Met Val Lys Pro Glu Asp Ile Met Tyr Leu 190 195 200			627
cag ttt gat cac ttt gat ttc ata cac cca cct ctt aat ctt gag aag Gln Phe Asp His Phe Asp Phe Ile His Pro Pro Leu Asn Leu Glu Lys 205 210 215			675
tct att caa gca tct atg gta ata agc ttt gag aga ata aat tat atc Ser Ile Gln Ala Ser Met Val Ile Ser Phe Glu Arg Ile Asn Tyr Ile 220 225 230			723
aaa cga tgc atg atg gaa gaa tgc aaa gaa ttt ttt tct gca ttt gaa Lys Arg Cys Met Met Glu Glu Cys Lys Glu Phe Phe Ser Ala Phe Glu 235 240 245 250			771
gtt gta gta gca ttg att tgg ctg gca agg aca aag tct ttt cga att Val Val Val Ala Leu Ile Trp Leu Ala Arg Thr Lys Ser Phe Arg Ile 255 260 265			819
cca ccc aat gag tat gtg aaa att atc ttt cca atc gac atg agg aat Pro Pro Asn Glu Tyr Val Lys Ile Ile Phe Pro Ile Asp Met Arg Asn 270 275 280			867
tca ttt gac tcc cct ctt cca aag gga tac tat ggt aat gct att ggt Ser Phe Asp Ser Pro Leu Pro Lys Gly Tyr Tyr Gly Asn Ala Ile Gly 285 290 295			915

aat gca tgt gca atg gat aat gtc aaa gac ctc tta aat gga tct ctt 963
 Asn Ala Cys Ala Met Asp Asn Val Lys Asp Leu Leu Asn Gly Ser Leu
 300 305 310

tta tat gct cta atg ctt ata aag aaa tca aag ttt gct tta aat gag 1011
 Leu Tyr Ala Leu Met Leu Ile Lys Lys Ser Lys Phe Ala Leu Asn Glu
 315 320 325 330

aat ttc aaa tca aga atc ttg aca aaa cca tct aca tta gat gcg aat 1059
 Asn Phe Lys Ser Arg Ile Leu Thr Lys Pro Ser Thr Leu Asp Ala Asn
 335 340 345

atg aag cat gaa aat gta gtc gga tgt ggc gat tgg agg aat ttg gga 1107
 Met Lys His Glu Asn Val Val Gly Cys Gly Asp Trp Arg Asn Leu Gly
 350 355 360

ttt tat gaa gca gat ttt gga tgg gga aat gca gtg aat gta agc ccc 1155
 Phe Tyr Glu Ala Asp Phe Gly Trp Gly Asn Ala Val Asn Val Ser Pro
 365 370 375

atg cag caa caa aga gag cat gaa tta gct atg caa aat tat ttt ctt 1203
 Met Gln Gln Gln Arg Glu His Glu Leu Ala Met Gln Asn Tyr Phe Leu
 380 385 390

ttt ctc cga tca gct aag aac atg att gat gga atc aag ata cta atg 1251
 Phe Leu Arg Ser Ala Lys Asn Met Ile Asp Gly Ile Lys Ile Leu Met
 395 400 405 410

ttc atg cct gca tca atg gtg aaa cca ttc aaa att gaa atg gaa gtc 1299
 Phe Met Pro Ala Ser Met Val Lys Pro Phe Lys Ile Glu Met Glu Val
 415 420 425

aca ata aac aaa tat gtg gct aaa ata tgt aac tct aag tta taa 1344
 Thr Ile Asn Lys Tyr Val Ala Lys Ile Cys Asn Ser Lys Leu
 430 435 440

agtatgtatg actgcaaaat agtaaaatat tgcattggtgg atgc 1388

<210> 24
 <211> 440
 <212> PRT
 <213> *Taxus cuspidata*

<400> 24

Met Gly Arg Phe Asn Val Asp Met Ile Glu Arg Val Ile Val Ala Pro
1 5 10 15

Cys Leu Gln Ser Pro Lys Asn Ile Leu His Leu Ser Pro Ile Asp Asn
20 25 30

Lys Thr Arg Gly Leu Thr Asn Ile Leu Ser Val Tyr Asn Ala Ser Gln
35 40 45

Arg Val Ser Val Ser Ala Asp Pro Ala Lys Thr Ile Arg Glu Ala Leu
50 55 60

Ser Lys Val Leu Val Tyr Tyr Pro Pro Phe Ala Gly Arg Leu Arg Asn
65 70 75 80

Thr Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly Glu Gly Ala Val
85 90 95

Phe Val Glu Ala Met Ala Asp Asn Asp Leu Ser Val Leu Gln Asp Phe
100 105 110

Asn Glu Tyr Asp Pro Ser Phe Gln Gln Leu Val Phe Asn Leu Arg Glu
115 120 125

Asp Val Asn Ile Glu Asp Leu His Leu Leu Thr Val Gln Val Thr Arg
130 135 140

Phe Thr Cys Gly Gly Phe Val Val Gly Thr Arg Phe His His Ser Val
145 150 155 160

Ser Asp Gly Lys Gly Ile Gly Gln Leu Leu Lys Gly Met Gly Glu Met
165 170 175

Ala Arg Gly Glu Phe Lys Pro Ser Leu Glu Pro Ile Trp Asn Arg Glu
180 185 190

Met Val Lys Pro Glu Asp Ile Met Tyr Leu Gln Phe Asp His Phe Asp
195 200 205

Phe Ile His Pro Pro Leu Asn Leu Glu Lys Ser Ile Gln Ala Ser Met
210 215 220

Val Ile Ser Phe Glu Arg Ile Asn Tyr Ile Lys Arg Cys Met Met Glu
225 230 235 240

Glu Cys Lys Glu Phe Phe Ser Ala Phe Glu Val Val Val Ala Leu Ile
245 250 255

Trp Leu Ala Arg Thr Lys Ser Phe Arg Ile Pro Pro Asn Glu Tyr Val
260 265 270

Lys Ile Ile Phe Pro Ile Asp Met Arg Asn Ser Phe Asp Ser Pro Leu
275 280 285

Pro Lys Gly Tyr Tyr Gly Asn Ala Ile Gly Asn Ala Cys Ala Met Asp
290 295 300

Asn Val Lys Asp Leu Leu Asn Gly Ser Leu Leu Tyr Ala Leu Met Leu
 305 310 315 320

Ile Lys Lys Ser Lys Phe Ala Leu Asn Glu Asn Phe Lys Ser Arg Ile
 325 330 335

Leu Thr Lys Pro Ser Thr Leu Asp Ala Asn Met Lys His Glu Asn Val
 340 345 350

Val Gly Cys Gly Asp Trp Arg Asn Leu Gly Phe Tyr Glu Ala Asp Phe
 355 360 365

Gly Trp Gly Asn Ala Val Asn Val Ser Pro Met Gln Gln Gln Arg Glu
 370 375 380

His Glu Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu Arg Ser Ala Lys
 385 390 395 400

Asn Met Ile Asp Gly Ile Lys Ile Leu Met Phe Met Pro Ala Ser Met
 405 410 415

Val Lys Pro Phe Lys Ile Glu Met Glu Val Thr Ile Asn Lys Tyr Val
 420 425 430

Ala Lys Ile Cys Asn Ser Lys Leu
 435 440

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> modified_base
 <222> (6)..(6)
 <223> I

<220>
 <221> modified_base
 <222> (9)..(9)
 <223> I

<220>
 <221> modified_base
 <222> (14)..(14)
 <223> I

<400> 25
ttymgncna gmgnttygar

20

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
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<222> (6)..(6)
<223> I

<220>
<221> modified_base
<222> (9)..(9)
<223> I

<220>
<221> modified_base
<222> (12)..(12)
<223> I

<220>
<221> modified_base
<222> (15)..(15)
<223> I

<400> 26
ttymgnccnt cnmgnttyga r

21

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (3)..(6)
<223> I

<220>
<221> modified_base
<222> (9)..(9)
<223> I

<220>
<221> modified_base
<222> (12)..(12)
<223> I

<220>
<221> modified_base
<222> (18)..(18)
<223> I

<400> 27
cknnnnccng cncraangg

20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (12)..(12)
<223> I

<220>
<221> modified_base
<222> (15)..(15)
<223> I

<400> 28
gargarttym gnccngarmg

20

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (10)..(12)
<223> I

<220>
<221> modified_base
<222> (15)..(15)
<223> I

<220>
<221> modified_base
<222> (18)..(18)
<223> I

<400> 29
garaarttyn nncnganar gtty

24

<210> 30

<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (6)..(9)
<223> I

<220>
<221> modified_base
<222> (12)..(15)
<223> I

<220>
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<222> (18)..(18)
<223> I

<220>
<221> modified_base
<222> (21)..(21)
<223> I

<220>
<221> modified_base
<222> (27)..(27)
<223> I

<400> 30
ggrcannnnc knnnnccncc nccraangg

29

<210> 31
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (3)..(3)
<223> I

<220>
<221> modified_base
<222> (9)..(9)
<223> I

<220>
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<222> (12)..(12)
<223> I

<220>
 <221> modified_base
 <222> (18)..(18)
 <223> I

<220>
 <221> modified_base
 <222> (21)..(21)
 <223> I

<220>
 <221> modified_base
 <222> (24)..(24)
 <223> I

<220>
 <221> modified_base
 <222> (30)..(30)
 <223> I

<400> 31
 ccnggrcana tnmkyytncc ngcnccraan gg 32

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 32
 atggacgccc tgtataagag 20

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 33
 tcaattgact atggtctcgg 20

<210> 34
 <211> 1488
 <212> DNA
 <213> Taxus cuspidata

<220>
 <221> CDS
 <222> (24)..(1346)
 <223> coding sequence

<400> 34
 gcaccagctg agcttgatct gag atg gca ggc tca aca gaa ttt gtg gta aga 53

Met Ala Gly Ser Thr Glu Phe Val Val Arg																
1 5 10																
agc tta gag aga gtg atg gtg gct cca agc cag cca tcg ccc aaa gct	101															
Ser Leu Glu Arg Val Met Val Ala Pro Ser Gln Pro Ser Pro Lys Ala																
	15 20 25															
ttc ctg cag ctc tcc acc ctt gac aat cta cca ggg gtg aga gaa aac	149															
Phe Leu Gln Leu Ser Thr Leu Asp Asn Leu Pro Gly Val Arg Glu Asn																
	30 35 40															
att ttt aac acc ttg tta gtc tac aat gcc tca gac aga gtt tcc gta	197															
Ile Phe Asn Thr Leu Leu Val Tyr Asn Ala Ser Asp Arg Val Ser Val																
	45 50 55															
gat cct gca aaa gta att cgg cag gct ctc tcc aag gtg ttg gtg tac	245															
Asp Pro Ala Lys Val Ile Arg Gln Ala Leu Ser Lys Val Leu Val Tyr																
	60 65 70															
tat tcc cct ttt gca ggg cgt ctc agg aaa aaa gaa aat gga gat ctt	293															
Tyr Ser Pro Phe Ala Gly Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu																
	75 80 85 90															
gaa gtg gag tgc aca ggg gag ggt gct ctg ttt gtg gaa gcc atg gct	341															
Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Met Ala																
	95 100 105															
gac act gac ctc tca gtc tta gga gat ttg gat gac tac agt cct tca	389															
Asp Thr Asp Leu Ser Val Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser																
	110 115 120															
ctt gag caa cta ctt ttt tgt ctt ccg cct gat aca gat att gag gac	437															
Leu Glu Gln Leu Leu Phe Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp																
	125 130 135															
atc cat cct ctg gtg gtt cag gta act cgt ttt aca tgt gga ggt ttt	485															
Ile His Pro Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe																
	140 145 150															
gtt gta ggg gtg agt ttc tgc cat ggt ata tgt gat gga cta gga gca	533															
Val Val Gly Val Ser Phe Cys His Gly Ile Cys Asp Gly Leu Gly Ala																
	155 160 165 170															
ggc cag ttt ctt ata gcc atg gga gag atg gca agg gga gag att aag	581															
Gly Gln Phe Leu Ile Ala Met Gly Glu Met Ala Arg Gly Glu Ile Lys																
	175 180 185															
ccc tcc tcg gag cca ata tgg aag aga gaa ttg ctg aag ccg gaa gac	629															
Pro Ser Ser Glu Pro Ile Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp																
	190 195 200															
cct tta tac cgg ttc cag tat tat cac ttt caa ttg att tgc ccg cct	677															
Pro Leu Tyr Arg Phe Gln Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro																
	205 210 215															
tca aca ttc ggg aaa ata gtt caa gga tct ctt gtt ata acc tct gag	725															
Ser Thr Phe Gly Lys Ile Val Gln Gly Ser Leu Val Ile Thr Ser Glu																
	220 225 230															
aca ata aat tgt atc aaa caa tgc ctt agg gaa gaa agt aaa gaa ttt	773															
Thr Ile Asn Cys Ile Lys Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe																

235	240	245	250	
tgc tct gcg ttc gaa gtt gta tct gca ttg gct tgg ata gca agg aca				821
Cys Ser Ala Phe	Glu Val Val Ser Ala	Leu Ala Trp Ile	Ala Arg Thr	
	255	260	265	
agg gct ctt caa att cca cat agt gag aat gtg aag ctt att ttt gca				869
Arg Ala Leu Gln Ile Pro His Ser	Glu Asn Val Lys	Leu Ile Phe	Ala	
	270	275	280	
atg gac atg aga aaa tta ttt aat cca cca ctt tcg aag gga tac tac				917
Met Asp Met Arg Lys Leu Phe	Asn Pro Pro Leu Ser	Lys Gly Tyr Tyr		
	285	290	295	
ggg aat ttt gtt ggt acc gta tgt gca atg gat aat gtc aag gac cta				965
Gly Asn Phe Val Gly Thr Val Cys Ala Met Asp	Asn Val Lys Asp	Leu		
	300	305	310	
tta agt gga tct ctt ttg cgt gtt gta agg att ata aag aaa gca aag				1013
Leu Ser Gly Ser Leu Leu Arg Val Val Arg Ile Ile Lys Lys Ala Lys				
	315	320	325	330
gtc tct tta aat gag cat ttc acg tca aca atc gtg aca ccc cgt tct				1061
Val Ser Leu Asn Glu His Phe Thr Ser Thr Ile Val Thr Pro Arg Ser				
	335	340	345	
gga tca gat gag agt atc aat tat gaa aac ata gtt gga ttt ggt gat				1109
Gly Ser Asp Glu Ser Ile Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp				
	350	355	360	
cga agg cga ttg gga ttt gat gaa gta gac ttt ggg tgg ggg cat gca				1157
Arg Arg Arg Leu Gly Phe Asp Glu Val Asp Phe Gly Trp Gly His Ala				
	365	370	375	
gat aat gta agt ctc gtg caa cat gga ttg aag gat gtt tca gtc gtg				1205
Asp Asn Val Ser Leu Val Gln His Gly Leu Lys Asp Val Ser Val Val				
	380	385	390	
caa agt tat ttt ctt ttc ata cga cct ccc aag aat aac ccc gat gga				1253
Gln Ser Tyr Phe Leu Phe Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly				
	395	400	405	410
atc aag atc cta tcg ttc atg ccc ccg tca ata gtg aaa tcc ttc aaa				1301
Ile Lys Ile Leu Ser Phe Met Pro Pro Ser Ile Val Lys Ser Phe Lys				
	415	420	425	
ttt gaa atg gaa acc atg aca aac aaa tat gta act aag cct tga				1346
Phe Glu Met Glu Thr Met Thr Asn Lys Tyr Val Thr Lys Pro				
	430	435	440	
aattgtagta acttaagcct tgcattttca gaataagttt tggcactggg ttgtgggtga				1406
agtaatgtac ttttgaattt tgatttaaag ttctattcaa agttataaaa tgtattatgt				1466
gaaaatatgt tgcaattatg gt				1488
<p><210> 35 <211> 440 <212> PRT <213> <i>Taxus cuspidata</i></p>				

<400> 35

Met Ala Gly Ser Thr Glu Phe Val Val Arg Ser Leu Glu Arg Val Met
 1 5 10 15

Val Ala Pro Ser Gln Pro Ser Pro Lys Ala Phe Leu Gln Leu Ser Thr
 20 25 30

Leu Asp Asn Leu Pro Gly Val Arg Glu Asn Ile Phe Asn Thr Leu Leu
 35 40 45

Val Tyr Asn Ala Ser Asp Arg Val Ser Val Asp Pro Ala Lys Val Ile
 50 55 60

Arg Gln Ala Leu Ser Lys Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly
 65 70 75 80

Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly
 85 90 95

Glu Gly Ala Leu Phe Val Glu Ala Met Ala Asp Thr Asp Leu Ser Val
 100 105 110

Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser Leu Glu Gln Leu Leu Phe
 115 120 125

Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp Ile His Pro Leu Val Val
 130 135 140

Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
 145 150 155 160

Cys His Gly Ile Cys Asp Gly Leu Gly Ala Gly Gln Phe Leu Ile Ala
 165 170 175

Met Gly Glu Met Ala Arg Gly Glu Ile Lys Pro Ser Ser Glu Pro Ile
 180 185 190

Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp Pro Leu Tyr Arg Phe Gln
 195 200 205

Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro Ser Thr Phe Gly Lys Ile
 210 215 220

Val Gln Gly Ser Leu Val Ile Thr Ser Glu Thr Ile Asn Cys Ile Lys
 225 230 235 240

Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe Cys Ser Ala Phe Glu Val
 245 250 255

Val Ser Ala Leu Ala Trp Ile Ala Arg Thr Arg Ala Leu Gln Ile Pro
 260 265 270

His Ser Glu Asn Val Lys Leu Ile Phe Ala Met Asp Met Arg Lys Leu
 275 280 285

Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr Gly Asn Phe Val Gly Thr
 290 295 300

Val Cys Ala Met Asp Asn Val Lys Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320

Arg Val Val Arg Ile Ile Lys Lys Ala Lys Val Ser Leu Asn Glu His
 325 330 335

Phe Thr Ser Thr Ile Val Thr Pro Arg Ser Gly Ser Asp Glu Ser Ile
 340 345 350

Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp Arg Arg Arg Leu Gly Phe
 355 360 365

Asp Glu Val Asp Phe Gly Trp Gly His Ala Asp Asn Val Ser Leu Val
 370 375 380

Gln His Gly Leu Lys Asp Val Ser Val Val Gln Ser Tyr Phe Leu Phe
 385 390 395 400

Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly Ile Lys Ile Leu Ser Phe
 405 410 415

Met Pro Pro Ser Ile Val Lys Ser Phe Lys Phe Glu Met Glu Thr Met
 420 425 430

Thr Asn Lys Tyr Val Thr Lys Pro
 435 440

<210> 36
 <211> 1338
 <212> DNA
 <213> *Taxus cuspidata*

<220>

<221> CDS

<222> (1)..(1326)

<223> coding sequence

<400> 36

atg aag aag aca ggt tcg ttt gca gag ttc cat gtg aat atg att gag	48
Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu	
1 5 10 15	
cga gtc atg gtg aga ccg tgc ctg cct tcg ccc aaa aca atc ctc cct	96
Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro	
20 25 30	
ctc tcc gcc att gac aac atg gca aga gct ttt tct aac gta ttg ctg	144
Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu	
35 40 45	
gtc tac gct gcc aac atg gac aga gtc tct gca gat cct gca aaa gtg	192
Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val	
50 55 60	
att cga gag gct ctc tcc aag gtg ctg gtt tat tat tac cct ttt gct	240
Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala	
65 70 75 80	
ggg cgg ctc aga aat aaa gaa aat ggg gaa ctt gaa gtg gag tgc aca	288
Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr	
85 90 95	
ggg cag ggt gtt ctg ttt ctg gaa gcc atg gct gac agc gac ctt tca	336
Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser	
100 105 110	
gtc tta aca gat ctg gat aac tac aat cca tcg ttt cag cag ttg att	384
Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile	
115 120 125	
ttt tct cta cca cag gat aca gat att gag gac ctc cat ctc ttg att	432
Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile	
130 135 140	
gtt cag gta act cgt ttt aca tgt ggg ggt ttt gtt gtg gga gcg aat	480
Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn	
145 150 155 160	
gtg tat ggt agt gca tgc gat gca aaa gga ttt ggc cag ttt ctt caa	528
Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln	
165 170 175	
agt atg gca gag atg gcg aga gga gag gtt aag ccc tcg att gaa ccg	576
Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro	
180 185 190	
ata tgg aat aga gaa ctg gtg aag cta gaa cat tgt atg ccc ttc cgg	624
Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg	
195 200 205	
atg agt cat ctt caa att ata cat gca cct gta att gag gag aaa ttt	672
Met Ser His Leu Gln Ile Ile His Ala Pro Val Ile Glu Glu Lys Phe	
210 215 220	

gtt caa aca tct ctt gtt ata aac ttt gag ata ata aat cat atc aga 720
 Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile Ile Asn His Ile Arg
 225 230 235 240

cga cgc atc atg gaa gaa cgc aaa gaa agt tta tct tca ttt gaa att 768
 Arg Arg Ile Met Glu Glu Arg Lys Glu Ser Leu Ser Ser Phe Glu Ile
 245 250 255

gta gca gca ttg gtt tgg cta gca aag ata aag gct ttt caa att cca 816
 Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys Ala Phe Gln Ile Pro
 260 265 270

cat agt gag aat gtg aag ctt ctt ttt gca atg gac ttg agg aga tca 864
 His Ser Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Arg Ser
 275 280 285

ttt aat ccc cct ctt cca cat gga tac tat ggc aat gcc ttt ggt att 912
 Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly Asn Ala Phe Gly Ile
 290 295 300

gca tgt gca atg gat aat gtc cat gac ctt cta agt gga tct ctt ttg 960
 Ala Cys Ala Met Asp Asn Val His Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320

cgc act ata atg atc ata aag aaa tca aag ttc tct tta cac aaa gaa 1008
 Arg Thr Ile Met Ile Ile Lys Lys Ser Lys Phe Ser Leu His Lys Glu
 325 330 335

ctc aac tca aaa acc gtg atg agc tca tct gta gta gat gtc aat acg 1056
 Leu Asn Ser Lys Thr Val Met Ser Ser Ser Val Val Asp Val Asn Thr
 340 345 350

aag ttt gaa gat gta gtt tca att agt gat tgg agg cat tct ata tat 1104
 Lys Phe Glu Asp Val Val Ser Ile Ser Asp Trp Arg His Ser Ile Tyr
 355 360 365

tat gaa gtg gac ttt ggg tgg gga gat gca atg aac gtg agc act atg 1152
 Tyr Glu Val Asp Phe Gly Trp Gly Asp Ala Met Asn Val Ser Thr Met
 370 375 380

cta caa caa cag gag cac gag aaa tct ctg cca act tat ttt tct ttc 1200
 Leu Gln Gln Gln Glu His Glu Lys Ser Leu Pro Thr Tyr Phe Ser Phe
 385 390 395 400

cta caa tct act aag aac atg cca gat gga atc aag atg cta atg ttt 1248
 Leu Gln Ser Thr Lys Asn Met Pro Asp Gly Ile Lys Met Leu Met Phe
 405 410 415

atg cct cca tca aaa ctg aaa aaa ttc aaa att gaa ata gaa gct atg 1296
 Met Pro Pro Ser Lys Leu Lys Lys Phe Lys Ile Glu Ile Glu Ala Met
 420 425 430

ata aaa aaa tat gtg act aaa gtg tgt ccg tcaaagttat ga 1338
 Ile Lys Lys Tyr Val Thr Lys Val Cys Pro
 435 440

<210> 37
 <211> 442
 <212> PRT
 <213> Taxus cuspidata

<400> 37

Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu
 1 5 10 15

Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro
 20 25 30

Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu
 35 40 45

Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val
 50 55 60

Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala
 65 70 75 80

Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95

Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser
 100 105 110

Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile
 115 120 125

Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile
 130 135 140

Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn
 145 150 155 160

Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln
 165 170 175

Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro
 180 185 190

Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg
 195 200 205

Met Ser His Leu Gln Ile Ile His Ala Pro Val Ile Glu Glu Lys Phe
 210 215 220

Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile Ile Asn His Ile Arg
 225 230 235 240

Arg Arg Ile Met Glu Glu Arg Lys Glu Ser Leu Ser Ser Phe Glu Ile
 245 250 255

Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys Ala Phe Gln Ile Pro
 260 265 270

His Ser Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Arg Ser
 275 280 285

Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly Asn Ala Phe Gly Ile
 290 295 300

Ala Cys Ala Met Asp Asn Val His Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320

Arg Thr Ile Met Ile Ile Lys Lys Ser Lys Phe Ser Leu His Lys Glu
 325 330 335

Leu Asn Ser Lys Thr Val Met Ser Ser Ser Val Val Asp Val Asn Thr
 340 345 350

Lys Phe Glu Asp Val Val Ser Ile Ser Asp Trp Arg His Ser Ile Tyr
 355 360 365

Tyr Glu Val Asp Phe Gly Trp Gly Asp Ala Met Asn Val Ser Thr Met
 370 375 380

Leu Gln Gln Gln Glu His Glu Lys Ser Leu Pro Thr Tyr Phe Ser Phe
 385 390 395 400

Leu Gln Ser Thr Lys Asn Met Pro Asp Gly Ile Lys Met Leu Met Phe
 405 410 415

Met Pro Pro Ser Lys Leu Lys Lys Phe Lys Ile Glu Ile Glu Ala Met
 420 425 430

Ile Lys Lys Tyr Val Thr Lys Val Cys Pro
 435 440

<210> 38
 <211> 1326
 <212> DNA
 <213> *Taxus canadensis*

<220>

<221> CDS
 <222> (1)..(1326)
 <223> coding sequence

<400> 38

atg gag aag gca ggc tca aca gac ttc cat gta aag aaa ttt gat cca	48
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1 5 10 15	
gtc atg gta gcc cca agc ctt cca tcg ccc aaa gct acc gtc cag ctc	96
Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu	
20 25 30	
tct gtc gtt gat agc cta aca atc tgc agg gga att ttt aac acg ttg	144
Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu	
35 40 45	
ttg gtt ttc aat gcc cct gac aac att tct gca gat cct gta aaa ata	192
Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile	
50 55 60	
att aga gag gct ctc tcc aag gtg ttg gtg tat tat ttc cct ctt gct	240
Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala	
65 70 75 80	
ggg cgg ctc aga agt aaa gaa att ggg gaa ctt gaa gtg gag tgc aca	288
Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr	
85 90 95	
ggg gat ggt gct ctg ttt gtg gaa gcc atg gtg gaa gac acc att tca	336
Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser	
100 105 110	
gtc tta cga gat ctg gat gac ctc aat cca tca ttt cag cag tta gtt	384
Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val	
115 120 125	
ttt tgg cat cca ttg gac act gct att gag gat ctt cat ctt gtg att	432
Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile	
130 135 140	
gtt cag gta aca cgt ttt aca tgt ggg ggc att gcc gtt gga gtg act	480
Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr	
145 150 155 160	
ttg ccc cat agt gta tgt gat gga cgt gga gca gcc cag ttt gtt aca	528
Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr	
165 170 175	
gca ctg gca gag atg gcg agg gga gag gtt aag ccc tca cta gaa cca	576
Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro	
180 185 190	
ata tgg aat aga gaa ttg ttg aac cct gaa gac cct cta cat ctc cag	624
Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln	
195 200 205	
tta aat caa ttt gat tcg ata tgc cca cct cca atg ctg gag gaa ttg	672
Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro Met Leu Glu Glu Leu	
210 215 220	

ggt caa gct tct ttt gtt ata aac gtt gac acc ata gaa tat atg aag	720
Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr Ile Glu Tyr Met Lys	
225 230 235 240	
caa tgt gtc atg gag gaa tgt aat gaa ttt tgt tcg tct ttt gaa gta	768
Gln Cys Val Met Glu Glu Cys Asn Glu Phe Cys Ser Ser Phe Glu Val	
245 250 255	
gtg gca gca ttg gtt tgg ata gca cgg aca aag gct ctt caa att cca	816
Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys Ala Leu Gln Ile Pro	
260 265 270	
cat act gag aat gtg aag ctt ctc ttt gcg atg gat ttg agg aaa tta	864
His Thr Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Lys Leu	
275 280 285	
ttt aat ccc cca ctt cca aat gga tat tat ggt aat gcc att ggt act	912
Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly Asn Ala Ile Gly Thr	
290 295 300	
gca tat gca atg gat aat gtc caa gac ctc tta aat gga tct ctt ttg	960
Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu Asn Gly Ser Leu Leu	
305 310 315 320	
cgt gct ata atg att ata aaa aaa gca aag gct gat tta aaa gat aat	1008
Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala Asp Leu Lys Asp Asn	
325 330 335	
tat tcg agg tca agg gta gtt aca aac cca tat tca tta gat gtg aac	1056
Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Tyr Ser Leu Asp Val Asn	
340 345 350	
aag aaa tcc gac aac att ctt gca ttg agt gac tgg agg cgg ttg gga	1104
Lys Lys Ser Asp Asn Ile Leu Ala Leu Ser Asp Trp Arg Arg Leu Gly	
355 360 365	
ttt tat gaa gcc gat ttt ggg tgg gga ggt cca ctg aat gta agt tcc	1152
Phe Tyr Glu Ala Asp Phe Gly Trp Gly Gly Pro Leu Asn Val Ser Ser	
370 375 380	
ctg caa cgg ttg gaa aat gga ttg cct atg ttt agt act ttt cta tac	1200
Leu Gln Arg Leu Glu Asn Gly Leu Pro Met Phe Ser Thr Phe Leu Tyr	
385 390 395 400	
cta cta cct gcc aaa aac aag tct gat gga atc aag ctg cta ctg tct	1248
Leu Leu Pro Ala Lys Asn Lys Ser Asp Gly Ile Lys Leu Leu Leu Ser	
405 410 415	
tgt atg cca cca aca aca ttg aaa tca ttt aaa att gta atg gaa gct	1296
Cys Met Pro Pro Thr Thr Leu Lys Ser Phe Lys Ile Val Met Glu Ala	
420 425 430	
atg ata gag aaa tat gta agt aaa gtg tga	1326
Met Ile Glu Lys Tyr Val Ser Lys Val	
435 440	
<210> 39	
<211> 441	
<212> PRT	
<213> Taxus canadensis	

<400> 39

Met Glu Lys Ala Gly Ser Thr Asp Phe His Val Lys Lys Phe Asp Pro
 1 5 10 15

Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu
 20 25 30

Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu
 35 40 45

Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile
 50 55 60

Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala
 65 70 75 80

Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95

Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser
 100 105 110

Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val
 115 120 125

Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile
 130 135 140

Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr
 145 150 155 160

Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr
 165 170 175

Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro
 180 185 190

Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln
 195 200 205

Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro Met Leu Glu Glu Leu
 210 215 220

Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr Ile Glu Tyr Met Lys
 225 230 235 240

Gln Cys Val Met Glu Glu Cys Asn Glu Phe Cys Ser Ser Phe Glu Val
 245 250 255

Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys Ala Leu Gln Ile Pro
 260 265 270

His Thr Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Lys Leu
 275 280 285

Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly Asn Ala Ile Gly Thr
 290 295 300

Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu Asn Gly Ser Leu Leu
 305 310 315 320

Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala Asp Leu Lys Asp Asn
 325 330 335

Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Tyr Ser Leu Asp Val Asn
 340 345 350

Lys Lys Ser Asp Asn Ile Leu Ala Leu Ser Asp Trp Arg Arg Leu Gly
 355 360 365

Phe Tyr Glu Ala Asp Phe Gly Trp Gly Gly Pro Leu Asn Val Ser Ser
 370 375 380

Leu Gln Arg Leu Glu Asn Gly Leu Pro Met Phe Ser Thr Phe Leu Tyr
 385 390 395 400

Leu Leu Pro Ala Lys Asn Lys Ser Asp Gly Ile Lys Leu Leu Leu Ser
 405 410 415

Cys Met Pro Pro Thr Thr Leu Lys Ser Phe Lys Ile Val Met Glu Ala
 420 425 430

Met Ile Glu Lys Tyr Val Ser Lys Val
 435 440

<210> 40
 <211> 1488
 <212> DNA
 <213> *Taxus canadensis*

<220>

<221> CDS
 <222> (1)..(1488)
 <223> coding sequence

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<400> 40
atg gac gcc atg gat ctc aca gtt gca aag ttt aag gaa ttc acg cag      48
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cta cag tcc tct gct att ctt ctc act gtt gtt tct gga atc atc gtc      96
Leu Gln Ser Ser Ala Ile Leu Leu Thr Val Val Ser Gly Ile Ile Val
          20          25          30

atc gta atc ctg ctc ctc cgt tct aaa cgc cgc tcc tct ctc aaa ctt      144
Ile Val Ile Leu Leu Leu Arg Ser Lys Arg Arg Ser Ser Leu Lys Leu
          35          40          45

cct ccg ggg aaa tta ggc ctc cct ctc att ggg gaa tcg tta tca ttc      192
Pro Pro Gly Lys Leu Gly Leu Pro Leu Ile Gly Glu Ser Leu Ser Phe
          50          55          60

ctg tgg gct ctt cga tca aac aca ctc gaa cag ttt gtg gac aaa aga      240
Leu Trp Ala Leu Arg Ser Asn Thr Leu Glu Gln Phe Val Asp Lys Arg
65          70          75          80

gtg aag aaa tac ggc aat gtc ttc aag aca tcg tta ctt ggg caa ccc      288
Val Lys Lys Tyr Gly Asn Val Phe Lys Thr Ser Leu Leu Gly Gln Pro
          85          90          95

aca gta gta ctg tgt ggc gca gcc gga aac cgc cta att ctg tcg aac      336
Thr Val Val Leu Cys Gly Ala Ala Gly Asn Arg Leu Ile Leu Ser Asn
          100          105          110

cag gag aag ctg ttg agc cga acg gtg tcg gat cga gta gcg aaa ctg      384
Gln Glu Lys Leu Leu Ser Arg Thr Val Ser Asp Arg Val Ala Lys Leu
          115          120          125

acg ggt gat act tct att tcg gtt ata gcg gga gac agt cat cgc atc      432
Thr Gly Asp Thr Ser Ile Ser Val Ile Ala Gly Asp Ser His Arg Ile
          130          135          140

ata cgc gca gca gtt gca ggg ttt ttg ggg cca gca gga ctc aag att      480
Ile Arg Ala Ala Val Ala Gly Phe Leu Gly Pro Ala Gly Leu Lys Ile
145          150          155          160

cac att ggc gaa atg agc gca cat atc cga aat cat atc aac caa gta      528
His Ile Gly Glu Met Ser Ala His Ile Arg Asn His Ile Asn Gln Val
          165          170          175

tgg aag gga aaa gat gaa gtg aac gtg ctt agt ttg gca aga gag ctg      576
Trp Lys Gly Lys Asp Glu Val Asn Val Leu Ser Leu Ala Arg Glu Leu
          180          185          190

gtc ttc gcc atg tcg gcc agt ttg ttt tta aat ata aat gat aga gag      624
Val Phe Ala Met Ser Ala Ser Leu Phe Leu Asn Ile Asn Asp Arg Glu
          195          200          205

gaa cag cac caa ttg cat aag act ctc gaa act att ctt ccc gga tat      672
Glu Gln His Gln Leu His Lys Thr Leu Glu Thr Ile Leu Pro Gly Tyr
210          215          220

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ttt tct gtt cct ata aac ttc ccc gga ttt gcc ttt cgc aag gca ctg Phe Ser Val Pro Ile Asn Phe Pro Gly Phe Ala Phe Arg Lys Ala Leu 225 230 235 240	720
gag gga aac tcg aag cgt agg aaa cat ttc tct gtt tta caa gaa aag Glu Gly Asn Ser Lys Arg Arg Lys His Phe Ser Val Leu Gln Glu Lys 245 250 255	768
aga aga agg gat ctg agc gta ggg tta gca tcc cgc act cag gat ctg Arg Arg Arg Asp Leu Ser Val Gly Leu Ala Ser Arg Thr Gln Asp Leu 260 265 270	816
ctt tct gtt ttg ctc gcc tac gaa gat gac aaa ggg aat cca ctc acc Leu Ser Val Leu Leu Ala Tyr Glu Asp Asp Lys Gly Asn Pro Leu Thr 275 280 285	864
gat gag gag gtc ctc gac aac att tct gcg ctc att gat ggc tcc tac Asp Glu Glu Val Leu Asp Asn Ile Ser Ala Leu Ile Asp Gly Ser Tyr 290 295 300	912
gag agc acc tct tca caa atg gcc atg ctt tta aag ctg ttg tct gac Glu Ser Thr Ser Ser Gln Met Ala Met Leu Leu Lys Leu Leu Ser Asp 305 310 315 320	960
cat cca gaa tgc tat gaa aaa gta gtt caa gag caa ttg gag ata gct His Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Glu Ile Ala 325 330 335	1008
tca cat aaa aag gaa gga gaa gaa atc aca tgg aag gat gtg aaa gcc Ser His Lys Lys Glu Gly Glu Glu Ile Thr Trp Lys Asp Val Lys Ala 340 345 350	1056
atg aga tac aca tgg caa gta atg cag gag acg ctg cgg atg ttt gcc Met Arg Tyr Thr Trp Gln Val Met Gln Glu Thr Leu Arg Met Phe Ala 355 360 365	1104
cct gtt ttt gga cct cga ggg aaa gct ata act gac att cat tat gac Pro Val Phe Gly Pro Arg Gly Lys Ala Ile Thr Asp Ile His Tyr Asp 370 375 380	1152
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acc cat cag aat gat aca tat ttc aat gag ccg gac aaa ttc atg ccg Thr His Gln Asn Asp Thr Tyr Phe Asn Glu Pro Asp Lys Phe Met Pro 405 410 415	1248
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Tyr Thr Pro Ile Asp Pro His Glu Ser Ile Trp Gly Arg Pro Leu Pro
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 Pro Pro Gly Lys Leu Gly Leu Pro Leu Ile Gly Glu Ser Leu Ser Phe
 50 55 60
 Leu Trp Ala Leu Arg Ser Asn Thr Leu Glu Gln Phe Val Asp Lys Arg
 65 70 75 80
 Val Lys Lys Tyr Gly Asn Val Phe Lys Thr Ser Leu Leu Gly Gln Pro
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 Thr Val Val Leu Cys Gly Ala Ala Gly Asn Arg Leu Ile Leu Ser Asn
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 Gln Glu Lys Leu Leu Ser Arg Thr Val Ser Asp Arg Val Ala Lys Leu
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 Thr Gly Asp Thr Ser Ile Ser Val Ile Ala Gly Asp Ser His Arg Ile
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 Ile Arg Ala Ala Val Ala Gly Phe Leu Gly Pro Ala Gly Leu Lys Ile
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 His Ile Gly Glu Met Ser Ala His Ile Arg Asn His Ile Asn Gln Val
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 Trp Lys Gly Lys Asp Glu Val Asn Val Leu Ser Leu Ala Arg Glu Leu
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Val Phe Ala Met Ser Ala Ser Leu Phe Leu Asn Ile Asn Asp Arg Glu
 195 200 205

Glu Gln His Gln Leu His Lys Thr Leu Glu Thr Ile Leu Pro Gly Tyr
 210 215 220

Phe Ser Val Pro Ile Asn Phe Pro Gly Phe Ala Phe Arg Lys Ala Leu
 225 230 235 240

Glu Gly Asn Ser Lys Arg Arg Lys His Phe Ser Val Leu Gln Glu Lys
 245 250 255

Arg Arg Arg Asp Leu Ser Val Gly Leu Ala Ser Arg Thr Gln Asp Leu
 260 265 270

Leu Ser Val Leu Leu Ala Tyr Glu Asp Asp Lys Gly Asn Pro Leu Thr
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Asp Glu Glu Val Leu Asp Asn Ile Ser Ala Leu Ile Asp Gly Ser Tyr
 290 295 300

Glu Ser Thr Ser Ser Gln Met Ala Met Leu Leu Lys Leu Leu Ser Asp
 305 310 315 320

His Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Glu Ile Ala
 325 330 335

Ser His Lys Lys Glu Gly Glu Glu Ile Thr Trp Lys Asp Val Lys Ala
 340 345 350

Met Arg Tyr Thr Trp Gln Val Met Gln Glu Thr Leu Arg Met Phe Ala
 355 360 365

Pro Val Phe Gly Pro Arg Gly Lys Ala Ile Thr Asp Ile His Tyr Asp
 370 375 380

Gly Tyr Thr Ile Pro Lys Gly Trp Gln Leu Ser Trp Ala Thr Tyr Ser
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Thr His Gln Asn Asp Thr Tyr Phe Asn Glu Pro Asp Lys Phe Met Pro
 405 410 415

Ser Arg Phe Asp Glu Glu Gly Gly Arg Leu Ala Pro Tyr Thr Phe Val
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Pro Phe Gly Gly Gly Arg Arg Lys Cys Pro Gly Trp Glu Phe Ala Lys
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Thr Glu Ile Leu Leu Phe Val His His Phe Val Lys Thr Phe Ser Ala
450 455 460

Tyr Thr Pro Ile Asp Pro His Glu Ser Ile Trp Gly Arg Pro Leu Pro
465 470 475 480

Pro Val Pro Ala Asn Gly Phe Pro Ile Lys Leu Ile Ser Arg Ser
485 490 495